

## REMARKS/ARGUMENTS

### **1.     *Status of the claims***

Claims 40, 67, 68 and 75 are amended and claims 79-80 are added. Claims 40 and 66-80 are currently pending with entry of the Amendment.

### **2.     *Support for the Amendments***

Support for the amendments to the claims can be found throughout the specification, the drawings, and the claims as originally drafted. No new matter is added.

### **3.     *Interview***

Applicants thank the Examiner for the helpful interview on December 18, 2003. It is Applicant's understanding that with the information provided herein, the amended claims are allowable.

### **4.     *Drawings***

Per the Examiner's request, Applicants have canceled Figure 9 and replaced it with the identical sequence labeled as Figure 8.

### **5.     *Obviousness-type double patenting rejection***

The Examiner rejected claims 40 and 66-78 under the judicially-created doctrine of obviousness-type double patenting over claims 1-18 of U.S. Patent No. 6,541,683. Applicants submit with this Amendment a terminal disclaimer of the term of a patent granted on the instant application over U.S. Patent No. 6,541,683. Applicants note that the filing of a terminal disclaimer to obviate a rejection based on non-statutory double patenting is not an admission of the propriety of the rejection. *See*, MPEP §804.02. Accordingly, Applicants respectfully request withdrawal of the rejection.

**6. *Rejection under 35 U.S.C. § 112, second paragraph***

Claims 40 and 66-74 were rejected under 35 U.S. C. § 112, second paragraph.

First, the Examiner helpfully noted that claims 40 and 75 refer to a nucleic acid sequence rather than an amino acid sequence. As amended, the claims include a reference to SEQ ID NO:2, an amino acid sequence.

Second, the Examiner questioned whether claims 67 and 68 were directed to introduction of a second expression cassette or whether the recitation was intended to modify the polynucleotide in claim 40. As amended, the claims clearly are directed to the latter. Accordingly, Applicants respectfully request withdrawal of the rejection.

**7. *Rejections under 35 U.S.C. § 112, first paragraph***

The Examiner rejected claims 40, 66 and 69-74 as allegedly not enabled by the specification. Specifically, the Examiner argued that it was unclear what the exact endpoints of the K, I and C domains were. Second, the Examiner argued that many proteins have K, I or C domains and therefore may be suppressed upon expression of the recited transgenes. Applicants respectfully traverse the rejection.

Applicants submit that the endpoints of the AGL8 K, I and C domains were known to those of skill in the art as of the filing date of the present application. As described in the specification on page 20, AGL8 is made up of four domains: the MADS box, and the K, I and C domains. The boundaries of these domains were described in the art before the filing date of the present application. As evidence, Applicants submit Mandel and Yanofsky, *Plant Cell* 7:1763-1771 (1995) (Exhibit A). The sequence of the Arabidopsis AGL8 sequence provided in the present application is identical to the sequence set forth in Mandel and Yanofsky. On page 1164 of Mandel and Yanofsky, the sequence of AGL8 is displayed with the MADS-box and K domains underlined. The I domain is the amino acid sequence between the two underlined sequences and the C domain is the amino acid sequence after the underlined K domain. Therefore, those of skill in the art would have understood the boundaries of the K and C domain of AGL8 as of the filing date of the present patent application.

With regard to the question of which genes will be suppressed upon expression of sequences encoding a polypeptide at least 75% identical to the K or C domains, Applicants submit that only AGL8, or orthologs of AGL8 have been identified with sequence homology within the 75% cut-off recited in the claims. As evidence, Applicants have supplied BLAST searches of the nr library of Genbank using either the K domain (Exhibit B) or the C domain (Exhibit C) of AGL8. The BLAST searches demonstrate that the only sequences with at least 75% sequence identity to either domain are in AGL8 or AGL8 orthologs. Applicants note that AGL8 is now referred to in the literature as "FUL" and that some of the sequences containing sequences at least 75 % identical to the K or C domains of SEQ ID NO:2 are named "FUL."

In view of this evidence, Applicants submit that the introduction of the recited sequences into plants would only affect expression of the intended target. Moreover, even if other gene sequences were silenced in a plant, the desired phenotype would still likely occur. Accordingly, Applicants submit that the claims are enabled across their full scope and respectfully request withdrawal of the rejection.

### CONCLUSION

In view of the foregoing, Applicants believe all claims now pending in this Application are in condition for allowance and an action to that end is respectfully requested.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,



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60106993 v1

Please amend claims 40, 67, 68 and 75 and cancel claim 65 as follows.

This listing of claims will replace all prior versions, and listings of claims in the application.

**Listing of Claims:**

40. (Currently amended) A method of enhancing lignification in a vascular plant, comprising introducing into the vascular plant a plant promoter operably linked to an exogenous nucleic acid at least 50 base pairs long, wherein the exogenous nucleic acid encodes a polypeptide fragment at least 75% identical to the K, ~~V~~ or C domains of SEQ ID NO:1 ~~suppressing expression of an AGL8-like gene product comprising a polypeptide at least 75% 50% identical to SEQ ID NO:2 in said vascular plant, thereby suppressing expression of an AGL8-like gene product at least 50% identical to SEQ ID NO:2 and~~ enhancing lignification.

65. (Canceled)

66. (Previously added) The method of claim 40, wherein the AGL8-like gene product comprises SEQ ID NO:2.

67. (Currently amended) The method of claim 40, comprising introducing into the plant a promoter operatively linked in the sense orientation to a polynucleotide encoding a polypeptide at least 75% ~~50%~~ identical to SEQ ID NO:2, thereby suppressing expression of the AGL8-like gene product.

68. (Currently amended) The method of claim 40, comprising introducing into the plant a promoter operatively linked in the antisense orientation to a polynucleotide encoding a polypeptide at least 75% ~~50%~~ identical to SEQ ID NO:2, thereby suppressing expression of the AGL8-like gene product.

69. (Previously added) The method of claim 40, wherein said vascular plant is a woody plant.

70. (Previously added) The method of claim 69, wherein said woody plant is selected from the group consisting of Eucalyptus, cottonwood, alder, Douglas fir, Hemlock, pine and spruce.

RESEARCH ARTICLE

# The Arabidopsis *AGL8* MADS Box Gene Is Expressed in Inflorescence Meristems and Is Negatively Regulated by *APETALA1*

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**MADS box genes encode putative transcription factors that play important roles in plant and animal development. In plants, MADS box genes are involved in the early step of specifying floral meristem identity as well as the later step of determining the fate of floral organ primordia. Here, we describe the isolation and characterization of a new MADS box gene from Arabidopsis, designated *AGL8*. Although *AGL8* RNA does not accumulate during vegetative growth, it accumulates to high levels in the inflorescence apical meristem as well as in the inflorescence stem and cauline leaves. *AGL8* RNA is excluded from the young flower primordia that arise on the flanks of the inflorescence meristem but later accumulates in the walls of the developing carpels. The lack of *AGL8* RNA in floral meristems is due in part to the action of another MADS box gene, *APETALA1*, because *AGL8* RNA does accumulate in *apetala1* mutant flower primordia.**

## INTRODUCTION

Plant growth depends on meristems, which are groups of undifferentiated cells that give rise to the diverse parts of a plant. During the vegetative phase of Arabidopsis growth, the shoot apical meristem produces a small number of leaf primordia on its flanks that develop into a rosette. Responding to both environmental (e.g., temperature and light conditions) and internal (e.g., age) factors, flowering is induced. Upon floral induction, the vegetative apical meristem undergoes a transition into an inflorescence meristem that produces floral meristems on its flanks. In addition, secondary inflorescences begin to differentiate from the axils of preexisting leaf primordia (Hempel and Feldman, 1994). The increased elongation of internodes during the reproductive phase results in the separation of the basal rosette leaves from the later-arising cauline leaves. Floral meristems produce primordia in a whorled arrangement, in contrast to the inflorescence meristem, which produces primordia in a spiral. The different floral organs arise in precisely defined positions within four concentric whorls. These organs are, from the first (outermost) to the fourth (innermost) whorl, four sepals, four petals, six stamens, and two fused carpels.

Molecular and genetic studies have identified early-acting genes, such as *APETALA1* (*AP1*), *CAULIFLOWER* (*CAL*), and

*LEAFY* (*LFY*) (Mandel et al., 1992; Weigel et al., 1992; Kempin et al., 1995), that specify the identity of floral meristems. These studies have also identified later-acting genes, such as *APETALA2* (*AP2*), *APETALA3* (*AP3*), *PISTILLATA* (*PI*), and *AGAMOUS* (*AG*) (Yanofsky et al., 1990; Jack et al., 1992; Goto and Meyerowitz, 1993; Jofuku et al., 1994), that determine the fate of floral organ primordia. Some of these genes have been shown to play multiple roles in flower development, such as *AP1*, which is involved in specifying both floral meristem and organ identity (for reviews, see Weigel and Meyerowitz, 1994; Yanofsky, 1995).

Five of these genes, *AP1*, *CAL*, *AP3*, *PI*, and *AG*, belong to the MADS box family of regulatory genes. MADS box genes encode DNA binding proteins that have a conserved N-terminal domain that shares similarity with transcription factors from yeast and mammals (Schwarz-Sommer et al., 1990). The name MADS derives from the initials of the first isolated members of this family: M for *MCM1*, a yeast gene that encodes PRTF, a transcription factor that regulates mating type-specific genes; A for *AG*; D for *DEFICIENS*, the *AP3* homolog first isolated in Antirrhinum; and S for SRF, serum response factor, a transcriptional regulator of *c-fos* (Norman et al., 1988; Passmore et al., 1988; Sommer et al., 1990; Yanofsky et al., 1990). In addition, the plant MADS box genes encode a second domain, the K domain, which has structural homology with a coiled-coil domain present in keratin, and it is thought to be involved in protein-protein interactions (Ma et al., 1991). The C terminus is rich in acidic amino acids, characteristic of transactivation

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domains. MADS box genes in Arabidopsis have been referred to as *AGL* (*AG*-like) genes because their isolation followed the prior isolation of *AG*. A total of 17 MADS box genes have been isolated and characterized in Arabidopsis (Yanofsky et al., 1990; Ma et al., 1991; Jack et al., 1992; Mandel et al., 1992; Gotq and Meyerowitz, 1994; Kempin et al., 1995; Rounsley et al., 1995).

Here, we report the isolation and characterization of a new MADS box gene in Arabidopsis. It is designated *AGL8*. RNA blotting and in situ hybridization analyses suggest that *AGL8* may define a new class of gene that regulates inflorescence development. In addition, we characterize the regulatory interactions between *AGL8* and other genes involved in meristem and organ identity.

## RESULTS

### Sequence and Mapping of *AGL8*

A new Arabidopsis MADS box gene, designated *AGL8*, was isolated by reduced stringency hybridization with a probe specific for the *AGL3* MADS box (see Methods). The *AGL8* cDNAs contain a single long open reading frame as well as 5' and 3' untranslated regions and poly(A) tails of varying lengths (Figure 1). The predicted protein encoded by this cDNA has a calculated molecular mass of 27.5 kD, similar to previously characterized members of this family. This new *AGL*, like *AG* and the previously reported members of the family, has the highly conserved MADS domain. *AGL8* was placed on the Arabidopsis restriction fragment length polymorphism map (Hauge et al., 1993). *AGL8* maps on chromosome 5, ~1.5 centimorgans above *LFY* and 3 centimorgans below *cer3* (data not shown).

### RNA Analyses

As a start toward determining the pattern of *AGL8* expression, RNA from roots, inflorescence stems, cauline leaves, and flowers was used in RNA blot hybridizations. A cDNA fragment containing only the 3' end of the gene was used as a probe to avoid cross-hybridization due to homology with the MADS box region (Figure 2A). *AGL8* RNA was detected not only in floral tissues but also in stems and cauline leaves. No *AGL8* RNA was detected in roots (Figure 2B).

We also analyzed the levels of *AGL8* RNA in different mutant backgrounds to begin to determine possible interactions between this gene and the floral homeotic genes. RNAs from wild-type, *ap1-1*, *ap2-2*, *ap3-3*, *pi-2*, *ag-1*, and *ag-2* flowers were isolated and hybridized to the *AGL8*-specific probe. *AGL8* is expressed at similar levels in wild-type, *ap3-3*, and *pi-2* flowers. In contrast, *AGL8* RNA levels increase in *ap1-1* and *ap2-2* mutant flowers and decrease in *ag-1* and *ag-2* flower tissue (Figure 2C).

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CCCAGAGAGACATAAGAAAGAAAGAGAGAGAGATCTT
TGCTCATTTTCAGGGTTGTGGTTTCTCTCTCTCTGAGATTTCAGAGAGAGAGAT
1 ATGGGAGAGAGGTAGGGTTCACTGAGAGAGATAGAGACAGATCAATAGCCAGTTACT
1 M G R G R V O L K R I E N K I N R O V T
61 TTCTCAAGAGAGAGGTCTGGTTTCTCAAGAAAGCTCATGAGATCTCTCTCTCTGGAT
21 F S K R R S G L L L K K A H E I S V L C D
121 GCTGAGGTGCTCTCATCTCTCTCTCTCAAGAGCCAACTCTTGAATATTCACCGAC
41 A E V A L I V F S S K G K L F E Y S T D
181 TCTTCATGAGAGAGATCTTGAAGCTATGATCGCTATTTATATTCAGACAAACACTT
61 S C M E R I L E R Y D R Y L Y S D K Q L
241 GTTGGCGAGAGCTTTCACAAAGTGAAATTTGGTTCTAGACATCTTAAGCTCAGGCA
81 V G R D V S Q S E N W V L E H A K L K A
301 AGAGTTGAGGTACTTGAAGAACAAAGGAATTTTATGGGGAGAGATCTTGATTCGTTG
101 R V E V L E K N K R N F M G E D L D S L
361 AGCTTGAAGAGCTCCAAAGCTTGAGCATCAGCTGATCGCATTAAGAGCATTAGG
121 S L K R L O S L E H O L D A A I K S I R
421 TCAAGAAAGACCAAGCTATGTTGGAATCATATCTCGCGCTCCAGAGAGAGGATAAGCC
141 S R K N O A M F E S I S A L O K K A
481 TTGCAAGATCACAACATTCGCTCTCAAAAGATTAGAGAGAGAGAGAGAAACGGGT
161 L Q D H N N S L L K K I K E R E K K T G
541 CAGCAAGAGAGACATTTAGTCCAATGCTCCAACTCTTCTCTCACTTCTCTGCTCAATAC
181 Q Q E G Q L V Q C S N S S S V L L P Q Y
601 TGGTAACTCTCTCCAGAGATGCTCTTGTGAGAGAGTTGGGGAGAGAACGGTGTGCA
201 C V T S S R D G F V E R V G G E N G G A
661 TGTGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
221 S S L T E P N S L L P A W M L R P T T T
721 AACGATGAGAACTATCTCACTCTTTATAATATAATGATAATATAATTAATGTTTATATT
241 N E *
781 TTCATACATTCAGCAATTTTGTGACTTATCTCACTTATTAATACGATATGTTTAA
841 GCTAGTCATATTATATGATGATGAGAACTCGGTGTGAGAGAGATATACGTAAGCTATC
901 ATTAGATTCAGTCTGCTTTAAGAACAAAGATTATCTCTGTAATGATTCTCATGAAA
961 TAn

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Figure 1. Nucleotide and Deduced Amino Acid Sequences of the *AGL8* cDNA Clone.

The asterisk indicates a stop codon, and A<sub>n</sub> represents a poly(A) tail. The MADS box region is underlined from amino acids 2 to 56, and the K box region is underlined from amino acids 92 to 158. The *AGL8* cDNA sequence has been submitted to GenBank as accession number U33473.

### *AGL8* RNA Accumulates in Two Distinct Phases

The temporal and spatial pattern of *AGL8* expression was analyzed by RNA in situ hybridizations in wild-type inflorescences of Arabidopsis. *AGL8* RNA was first detected in the inflorescence meristem as soon as the plant switches from vegetative to reproductive development (Figures 3A and 3B). As the inflorescence stem elongates, *AGL8* RNA accumulates in the inflorescence meristem and in the stem (Figures 3C and 3D). Although *AGL8* RNA was detected in the apical inflorescence meristem, *AGL8* expression was not detected at the initial stages (1 and 2) of flower development (stages defined by Smyth et al., 1990), when the young floral primordia arise on the flanks of the inflorescence meristem (Figures 3C and 3D). At approximately stage 3, *AGL8* expression resumes in the center of the floral dome in the region that corresponds to the fourth whorl and is excluded from all other primordia and the pedicel

(Figures 3C and 3D). At later stages, *AGL8* expression becomes localized to the carpel walls, in the region that constitutes the valves of the ovary (Figures 3E to 3J). No *AGL8* RNA was detected in the ovules, style, stigmatic tissues, or the septum that divides the ovary.

#### *AGL8* Is Negatively Regulated by *AP1*

*AGL8* RNA accumulates in the inflorescence stem and meristem, and it is excluded from the floral meristem at the earliest stages of flower formation. The loss of *AGL8* expression coincides with the onset of expression of the meristem identity gene *AP1* (Mandel et al., 1992). Although *AP1* RNA is not expressed in the inflorescence meristem, *AP1* is expressed throughout the floral meristem during stages 1 and 2 of flower development, and at stage 3, *AP1* expression abates from the central dome due to the negative regulation by *AG* (Gustafson-Brown et al., 1994). At later stages, *AP1* expression becomes localized to sepals and petals. To determine whether *AP1* is responsible, at least in part, for the loss of expression of *AGL8* at the initial stages of flower development, we analyzed *AGL8* expression in an *ap1* mutant background. *ap1-1* mutant flowers, which have normal third and fourth whorl organs, have leaflike organs in the first whorl instead of sepals and lack petals in the second whorl. In the axils of first whorl organs, secondary flowers arise, which reiterate this phenotype, and tertiary flowers can arise in the axils of leaflike organs of secondary flowers (Irish and Sussex, 1990).

In *ap1-1* mutant inflorescences, *AGL8* RNA accumulates in the inflorescence meristem and in the carpel walls of developing flowers, as in the wild type. However, in contrast to the wild type, *AGL8* RNA accumulates in stage 1 and 2 flower primordia

in *ap1* mutants. Furthermore, *AGL8* RNA accumulates in the first whorl leaflike organs and throughout the floral pedicel (Figures 4A and 4B). Secondary flowers arising in the axils of first whorl organs show a similar pattern of *AGL8* expression. The expanded pattern of *AGL8* expression in *ap1* mutant flowers suggests that *AP1* negatively regulates *AGL8* in young flower primordia and in sepals (and perhaps in petals) later in flower development.

Although these studies provide insight into the regulation of *AGL8*, they fail to shed light on the factor(s) that prevents *AGL8* from being expressed in third whorl organs. One candidate for repressing *AGL8* expression in stamens is *AP3*, because *AP3* regulates organ identity in the second and third whorls (Jack et al., 1992). Flowers of *ap3-3* mutants have sepals in the first and second whorls and carpels in the third and fourth whorls. In the *ap3-3* mutant, *AGL8* RNA is not expressed during stages 1 and 2 of flower development. However, when its expression is reestablished during stage 3, the domain in the center of the floral meristem expands to what appears to correspond to the third and fourth whorls (Figures 4C and 4D). At later stages, *AGL8* RNA accumulates in the carpel walls of the third and fourth whorl organs (Figures 4E and 4F), and it is not expressed in first and second whorl sepals. These results suggest that *AP3* can formally be considered a negative regulator of *AGL8* in the third whorl.

#### *AGL8* Expression in *ag*, *ap2*, and *clavata1* (*clv1*) Mutant Backgrounds

To provide further insights into the regulation and function of *AGL8*, we analyzed the pattern of *AGL8* expression in other mutant tissues.

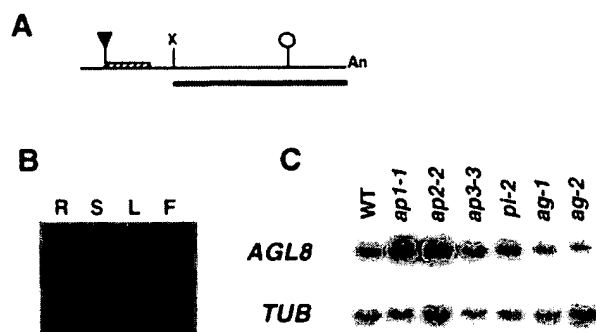


Figure 2. RNA Gel Blot Analyses of *AGL8*.

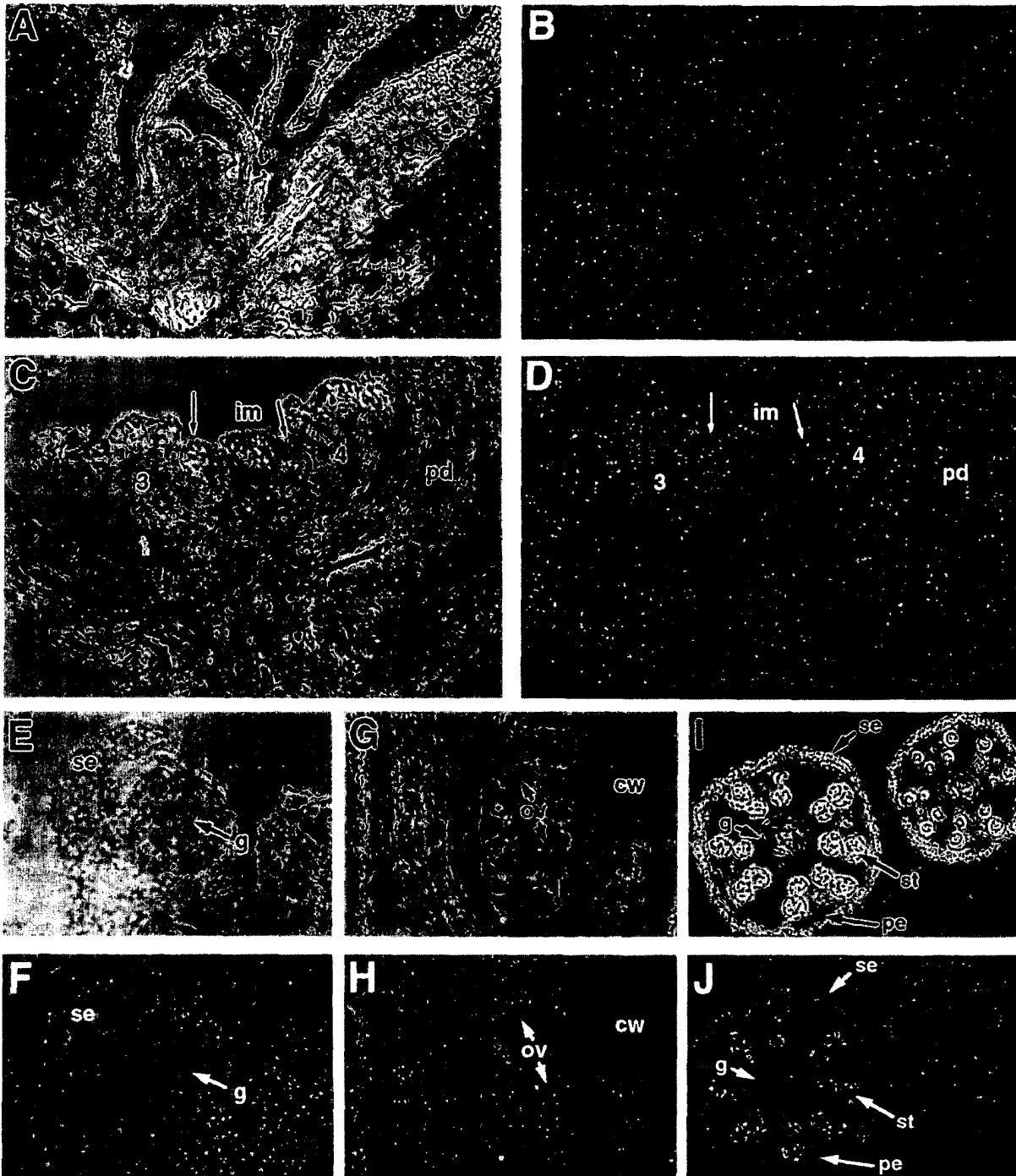
(A) Diagram of the *AGL8*-specific probe.  $\blacktriangledown$ , start codon;  $\circ$ , stop codon; hatched bar, MADS box; solid bar, probe; An, poly(A) tail; X, XbaI. (B) RNA blot hybridization of wild-type tissues with the *AGL8*-specific probe shown in (A). F, flowers; L, cauline leaves; R, roots; S, stems. (C) RNA gel blot hybridization of the wild type (WT) and different mutant floral tissues with *AGL8*. A tubulin (*TUB*) probe was used as a loading control (Marks et al., 1987).

#### *ag*

*ag-1* mutant flowers have petals replacing stamens in the third whorl, and the fourth whorl carpels are replaced by a new flower that reiterates the pattern (sepal, petal, petal)<sub>n</sub> (Bowman et al., 1991). *AGL8* RNA expression in *ag-1* mutants, as in the wild type, accumulates in the inflorescence meristem but not in the young flower primordia (Figures 4G and 4H). Even though carpels are not present in *ag* mutant flowers, *AGL8* RNA accumulates in the fourth whorl region of stage 3 flowers and continues to accumulate in the central meristematic region later in flower development (Figures 4I and 4J).

#### *ap2*

*ap2-2* mutant flowers have carpels in the first whorl instead of sepals, lack petals in the second whorl, and have fewer stamens in the third whorl, and the fourth whorl has normal or unfused carpels (Bowman et al., 1991). In this mutant, *AGL8* RNA is expressed in a similar way as in wild-type



**Figure 3.** *AGL8* Expression in Arabidopsis Wild-Type Tissues.

Longitudinal sections ([A] to [H]) and transverse sections ([I] and [J]) of wild-type plant tissues hybridized with the *AGL8*-specific antisense mRNA probe are shown. (A), (C), (E), (G), and (I) are bright-field micrographs of tissue sections. (B), (D), (F), (H), and (J) are bright/dark-field (red filter) double exposures.

(A) and (B) *AGL8* RNA accumulates in the inflorescence meristem at the apex of a wild-type plant immediately after the transition to flowering, 14 days post-germination under continuous light.

(C) and (D) A wild-type inflorescence. The arrows indicate floral meristems at stage 1 (right) and 2 (left). The other numbers indicate floral primordia at stages 3 and 4.

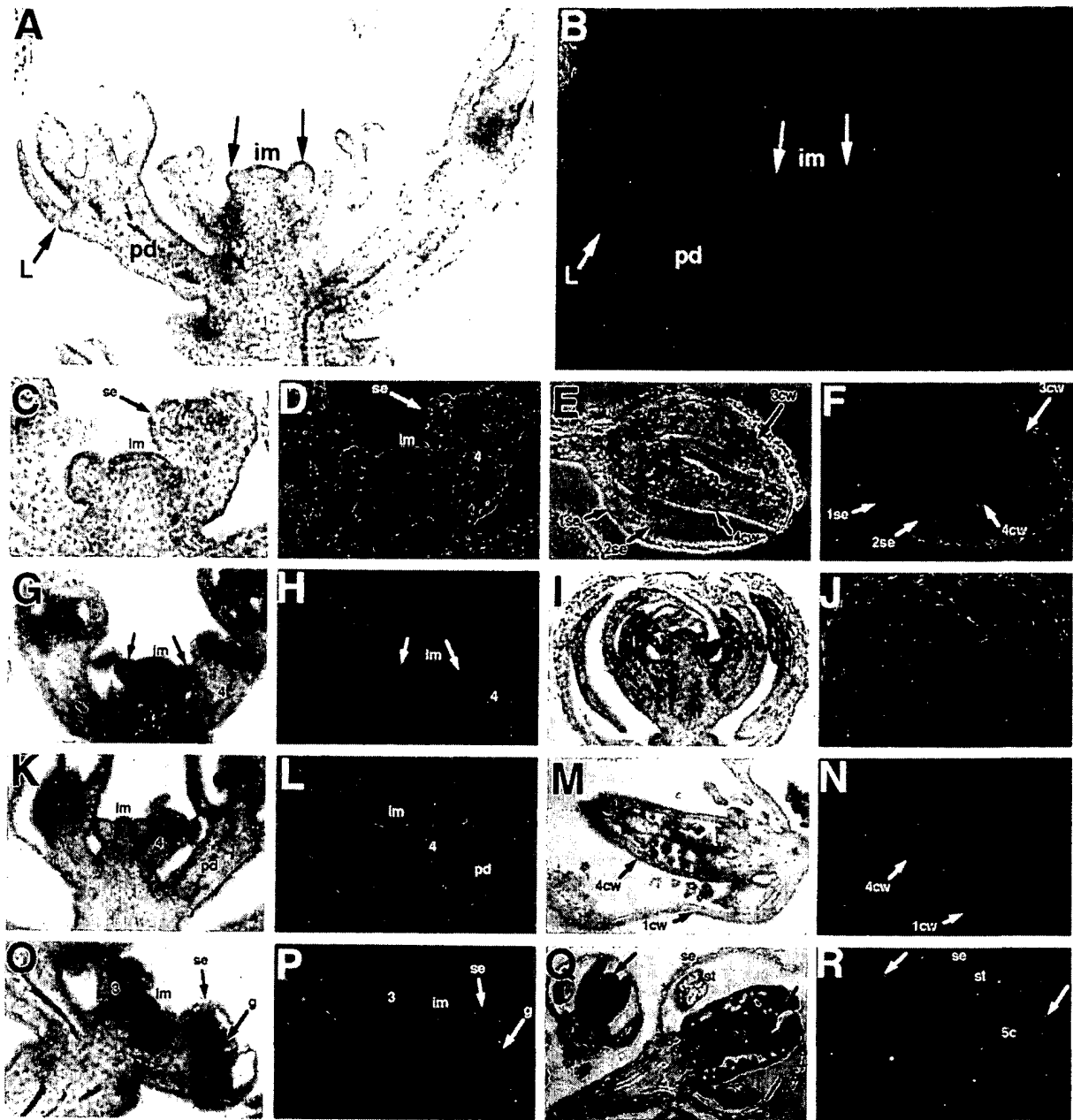
(E) and (F) A stage 7 flower.

(G) and (H) Part of a carpel of a stage 12 flower.

(I) and (J) Carpels of a stage 12 (left) and a stage 9 (right) flower.

cw, carpal wall; g, gynoecium; im, inflorescence meristem; ov, ovule; pd, pedicel; pe, petal; se, sepal; st, stamen.





**Figure 4.** *AGL8* Expression in the Floral Tissues of Mutants.

Longitudinal sections of floral tissues of mutants hybridized with the *AGL8*-specific antisense mRNA probe. (A), (C), (E), (G), (I), (K), (M), (O), and (Q) are bright-field micrographs. (B), (D), (F), (H), (J), (L), (N), (P), and (R) are bright/dark-field (red filter) double exposures.

(A) and (B) An *ap1-1* inflorescence. Arrows indicate two young floral primordia (stage 1 at left and stage 2 at right). Compare the expression of *AGL8* at similar stages of wild-type floral primordia.

(C) and (D) An *ap3-3* inflorescence with a stage 4 flower.

(E) and (F) An *ap3-3* flower at a later stage.

(G) and (H) An *ag-1* inflorescence. Arrows indicate two young floral primordia at stage 2 of flower development. A stage 4 flower is indicated.

(I) and (J) An older *ag-1* flower.

(K) and (L) An *ap2-2* inflorescence with a stage 4 flower.

(M) and (N) An older *ap2-2* flower.

(O) and (P) A *clv1-7* inflorescence with an approximately stage 3 floral primordium.

(Q) and (R) Two *clv1-4* flowers at different stages of development. The arrows indicate the tip of the fifth whorl carpel that shows no *AGL8* RNA accumulation.

g, gynoecium; im, inflorescence meristem; L, leaflike organ; pd, pedicel; se, sepal; st, stamen; 1cw, first whorl carpel; 1se, first whorl sepal; 2se, second whorl sepal; 3cw, third whorl carpel; 4cw, fourth whorl carpel; 5c, fifth whorl carpel.

inflorescences, and it is absent from stage 1 and 2 flower primordia (Figures 4K and 4L). Between stages 3 and 4, *AGL8* transcripts are detected in the center of the floral primordium and in pedicels (Figures 4K and 4L). At later stages, *AGL8* becomes localized to the carpel walls of both the first and fourth whorl carpel tissues (Figures 4M and 4N).

### *clv1*

*clv1* mutant plants have enlarged apical and floral meristems, displaying an array of different phenotypes that includes fasciation, disrupted phyllotaxis, and extra floral organs and whorls. *clv* mutant flowers have a fifth whorl that usually consists of extra carpelloid tissue (Clark et al., 1993). *AGL8* RNA is strongly expressed in the inflorescence stem and meristem of *clv* mutants, and it is turned off during stages 1 and 2 (Figures 4O and 4P). *AGL8* expression resumes in the center of the flower primordia of stage 3 flowers, as in the wild type (Figures 4O and 4P). At later stages, *AGL8* RNA accumulates in the carpel walls in the fourth whorl and throughout the carpelloid tissues that proliferate in the fifth whorl, except in an area located at the tip of these tissues (Figures 4Q and 4R).

## DISCUSSION

MADS box genes have been shown to play key roles in flower development, including the specification of floral meristem and floral organ identity. Here, we report the isolation and characterization of a new MADS box gene from Arabidopsis. We have designated it *AGL8*. Like other plant members of this family of genes, *AGL8* encodes a putative transcription factor that shares the highly conserved DNA binding MADS domain as well as the K domain, which is thought to be involved in protein-protein interactions (Ma et al., 1991). With this new member, the Arabidopsis MADS box family of genes includes at least 18 members.

In contrast to the majority of MADS box genes, which are expressed only in flowers, *AGL8* appears to be a novel MADS box gene whose RNA accumulates in two distinct phases of plant development. *AGL8* RNA was first detected immediately after the transition from vegetative to reproductive growth in the shoot apex. These data are supported by preliminary results using a 2.3-kb promoter fragment of *AGL8* fused to the  $\beta$ -glucuronidase (*GUS*) gene (Jefferson et al., 1987). Transgenic Arabidopsis plants harboring this construct showed no *GUS* activity during the vegetative phase of growth, but immediately after the transition to flowering, *GUS* activity was observed in the apical meristem and newly formed cauline leaves (M.A. Mandel and M.F. Yanofsky, unpublished observations). The high levels of *AGL8* RNA in the inflorescence meristem suggest a possible role for *AGL8* in maintaining inflorescence meristem identity or, alternatively, in promoting the initiation

of flowers. Genetic studies have identified a gene, *TERMINAL FLOWER (TFL)* (Shannon and Meeks-Wagner, 1991; Alvarez et al., 1992), that is proposed to play a role in maintaining the identity of the inflorescence meristem. This conclusion is inferred, in part, from the fact that the apical and lateral inflorescence meristems of *tfl* mutants develop as flowers. *AGL8* may interact with *TFL* to promote inflorescence development. Alternatively, *AGL8* could mediate the induction of the floral meristem identity genes, such as *AP1*, *CAL*, and *LFY*. We previously proposed a regulatory hierarchy of MADS box gene expression, beginning with the onset of the meristem identity genes *AP1* and *CAL* (Rounsley et al., 1995). The onset of *AGL8* expression in the inflorescence apical meristem immediately after the transition to flowering suggests that *AGL8* could act at the top of this hierarchy either by inducing or repressing the meristem identity genes.

In contrast to the high levels of *AGL8* RNA present in the inflorescence apical meristem, no *AGL8* RNA was detected in the flower primordia when they first arise on the flanks of the inflorescence meristem. This suggests that some factor(s) prevents *AGL8* expression early in flower development. One candidate for such a factor is the meristem identity gene *AP1*, whose expression pattern is largely complementary to that of *AGL8*, because *AP1* RNA is not detected in the inflorescence meristem but is detected in young flower primordia (Mandel et al., 1992). Consistent with this idea is the fact that *AGL8* RNA does accumulate in young flower primordia of the *ap1* mutant. Although the timing of the onset of *AP1* expression coincides with the corresponding loss of *AGL8* RNA accumulation, additional experiments are necessary to establish whether *AP1* represses *AGL8* through a direct or an indirect interaction. It is interesting to note that of 18 MADS box genes characterized in Arabidopsis, *AGL8* most closely resembles the floral meristem identity genes *AP1* and *CAL*, suggesting that *AGL8* has diverged relatively recently from these genes (Purugganan et al., 1995). This observation is particularly intriguing because these two classes of genes are expressed in inflorescence and floral meristems, respectively, and their expression patterns are complementary.

Although *AGL8* RNA is not expressed in young flower primordia, it does begin to accumulate later in flower development at about the time that sepal primordia begin to arise. This is also roughly the same time at which the organ identity genes *AP3*, *PI*, and *AG* begin to be expressed (Yanofsky et al., 1990; Drews et al., 1991; Jack et al., 1992; Goto and Meyerowitz, 1994). These data illustrate the two distinct phases of *AGL8* RNA accumulation, the first occurring during inflorescence development in the stem and cauline leaves and the second in the later stages of flower development. The expression of *AGL8* in the developing flowers is confined to the region from which the fourth whorl organ primordia later emerges. This is particularly evident as the flower begins to develop, because *AGL8* RNA accumulates throughout carpel primordia as they begin to form. Later in development, it is clear that *AGL8* RNA is specifically localized to the carpel walls and is absent from all other

cell types of the carpel. This feature distinguishes it from other characterized MADS box genes that are also expressed in carpels but whose RNAs accumulate in ovules (e.g., *AG*, *AGL2*, *AGL4*, *AGL5*, *AGL9*, *AGL11*, and *AGL13*) (Bowman et al., 1991b; Ma et al., 1991; Flannagan and Ma, 1994; Rounsley et al., 1995; Savidge et al., 1995; M.A. Mandel and M.F. Yanofsky, unpublished data).

The negative regulation of *AGL8* by *AP1* occurs not only in young flower primordia but also later in the developing organs and floral pedicel. This conclusion is based on the observation that *AGL8* RNA accumulates in the pedicel and first whorl leaflike organs in *ap1* mutant flowers and that *AGL8* is not expressed in the pedicel and first whorl organs in the wild type. *AP1* may also prevent *AGL8* expression in second whorl organs, although this is difficult to confirm because these organs fail to develop in *ap1* mutant plants. Although *AGL8* may be negatively regulated by *AP1* in sepals and petals, and *AGL8* is normally expressed in carpels, these data do not explain the lack of *AGL8* RNA in stamens. One candidate for a factor that prevents *AGL8* expression in third whorl organs is *AP3*, which is involved in specifying stamen identity (Jack et al., 1992). *AGL8* is expressed in the third whorl carpels that develop in *ap3* mutant flowers, consistent with the idea that *AP3* could act directly or indirectly to prevent *AGL8* expression in third whorl organs.

An interesting aspect of *AGL8* regulation arises from the analyses of *AGL8* RNA accumulation in *ag* mutants. RNA blot hybridizations showed decreased levels of *AGL8* RNA in *ag* mutant flowers. *ag* mutant flowers have only sepals and petals, and *AGL8* RNA does not accumulate in these organs in wild-type flowers. RNA *in situ* analyses of *ag* mutant flowers show that there is no expression of *AGL8* in sepals and petals but that *AGL8* is expressed in the meristematic region at the center of the flower. Because the center of the *ag* mutant flower continues to give rise to organ primordia, it is indeterminate, analogous in this sense to the inflorescence apical meristem, which is also indeterminate and continuously gives rise to flower primordia. *AGL8* may play a role in maintaining this indeterminacy.

Mutations in the *clv1* locus show a variety of phenotypes. They affect apical meristem size, cause fasciation, and in the strongest alleles, can alter the number of floral organs in all whorls and create additional whorls inside the carpels. Because the fifth whorl carpelloid organs that develop in *clv* mutants develop as an inflorescence in the *clv1 ap1* double mutant, it was suggested that *AP1* may be necessary to maintain the floral meristem identity of the inner region of *clv* mutant flowers (Clark et al., 1993). In *clv1* mutant flowers, *AGL8* RNA accumulates in the fourth whorl carpel walls and throughout the carpelloid tissue in the fifth whorl, except in the tip, where *AP1* is expressed. Perhaps the inflorescence character of the fifth whorl in *clv1 ap1* double mutant flowers is due in part to the activity of *AGL8*.

The isolation and characterization of *AGL8* reported here define a novel Arabidopsis MADS box gene that is one of the

earliest acting regulatory genes after the transition to flowering. These studies suggest that *AGL8* functions in the inflorescence apical meristem, perhaps to maintain inflorescence meristem identity. It will be interesting to determine whether *AGL8* interacts directly with other genes involved in early events in flower development and to identify and characterize loss-of-function alleles for this gene.

## METHODS

### Isolation of *AGL8*

A cosmid library of *Arabidopsis thaliana* Landsberg *erecta* genomic DNA (Yanofsky et al., 1990) was screened under reduced stringency conditions with a 550-bp *EcoRI* fragment of the cDNA clone of *AGL3* (for *AGAMOUS* [AG]-like; pCIT2280) that contains the MADS box (Ma et al., 1991). In addition to several clones that corresponded to *AGL3*, a new gene was identified and designated *AGL8*. An internal 264-bp *XbaI*-*PvuII* fragment of the *AGL8* gene containing the first exon and a portion of the first intron was used to screen, under stringent conditions, an ecotype Columbia cDNA library constructed with poly(A)<sup>+</sup> RNA from vegetative and floral tissues (Elledge et al., 1991), and two clones corresponding to *AGL8* were isolated.

The *AGL8* cDNA was excised from the  $\lambda$  YES vector using the reported procedure (Elledge et al., 1991) and subsequently subcloned into pGEM7Zi(+) (Promega). The cDNA clones were double-strand sequenced using the Sequenase Version 2.0 DNA sequencing kit (U.S. Biochemical Corp.) according to the manufacturer's protocol. Sequence analyses were performed using the Mac Vector program (International Biotechnologies, New Haven, CT).

### RNA Isolation and Blot Analyses

Total RNA from roots, stems, cauline leaves, and flowers (through stage 9) was isolated from wild-type Landsberg *erecta* plants and from flowers of different mutants according to Crawford et al. (1986). The RNA was size fractionated by gel electrophoresis under denaturing conditions in agarose gels with formaldehyde, transferred to Hybond-N membranes (Amersham Corp.), and hybridized according to standard procedures with <sup>32</sup>P-labeled specific probes. The *AGL8* probe used was an ~650 bp *XbaI*-*EcoRI* fragment of the 3' end of the cDNA clone (shown in Figure 2A). This probe did not contain any MADS box sequence.

### In Situ Hybridizations

Preparation of tissues and hybridization conditions were the same as previously described (Drews et al., 1991) with minor modifications. The *AGL8* <sup>35</sup>S-labeled antisense mRNA probe was synthesized with T7 RNA polymerase from a *Sall* digest of pAM497, which is a 580-bp subclone of the 3' end of the *AGL8* cDNA generated by polymerase chain reaction in the pCRII vector (Invitrogen, San Diego, CA). The probe was used at a final concentration of 2.5 × 10<sup>7</sup> cpm/mL. Slides were exposed for 4 to 5 weeks.

## Image Processing

Photographic slides were scanned and digitized using a Coolsan (Nikon Inc., Melville, NY). Additional processing was performed using Adobe Photoshop 2.5 (Adobe Systems Inc., Mountain View, CA). Composite figures were printed using a Tektronix Phaser IIsdx (Tektronix Inc., Wilsonville, OR) dye sublimation printer.

## ACKNOWLEDGMENTS

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## *results of* **BLAST**

**BLASTP 2.2.6 [Apr-09-2003]**

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1071780695-17291-67851912928.BLASTQ4

**Query=**

(84 letters)

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translations+PDB+SwissProt+PIR+PRF

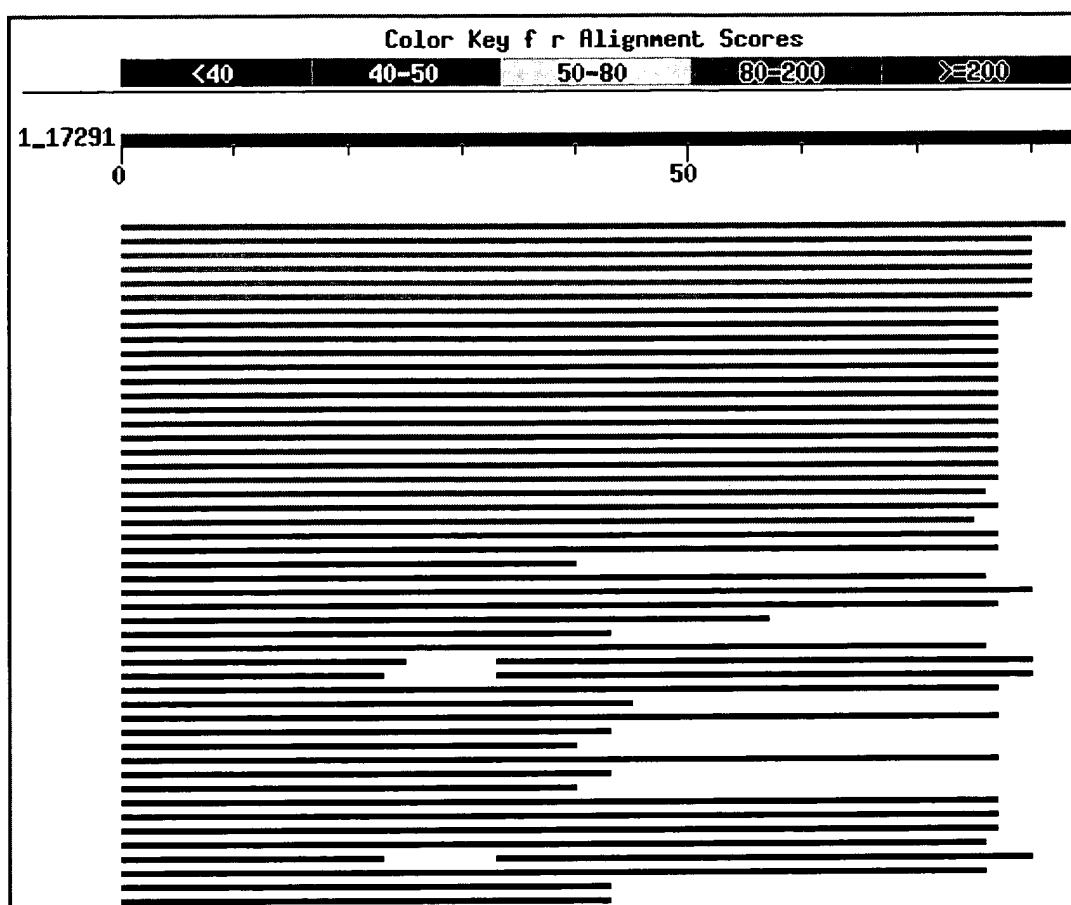
1,580,593 sequences; 517,909,209 total letters

If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQs](#)

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### Distribution of 52 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:				Score (bits)	E Value
gi 18424410 ref NP_568929.1	MADS-box protein [Arabidopsis ...	160	5e-39		
gi 23304672 emb CAD47849.1	MADS-box protein FUL-a [Brassic...	140	7e-33		
gi 23304674 emb CAD47850.1	MADS-box protein FUL-b [Brassic...	129	1e-29		
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gi 27373049 gb AAO12211.1	MADS11 [Nicotiana tabacum]	47	9e-05		
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## Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|18424410|ref|NP\_568929.1| MADS-box protein [Arabidopsis thaliana]  
 gi|3912998|sp|Q38876|AGL8 ARATH Agamous-like MADS box protein AGL8 (Floral homeot  
 (Transcription factor FRUITFULL)  
 gi|2129536|pir|S71208 MADS box protein AGL8 - Arabidopsis thaliana  
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Score = 160 bits (404), Expect = 5e-39

Identities = 84/84 (100%), Positives = 84/84 (100%)

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 Query: 61 GASSLTEPNSLLPAWMLRPTTTNE 84  
 GASSLTEPNSLLPAWMLRPTTTNE  
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☐ >gi|23304672|emb|CAD47849.1| MADS-box protein FUL-a [Brassica oleracea var. botrytis]  
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Identities = 71/81 (87%), Positives = 76/81 (93%)

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Query: 61 GASSLTEPNSLLPAWMLRPTT 81  
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☐ >gi|23304674|emb|CAD47850.1| MADS-box protein FUL-b [Brassica oleracea var. botrytis]  
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AS L EPNSLLPAWMLRPTT  
Sbjct: 219 VASLLAEPNSLLPAWMLRPTT 239

☐ >gi|3913000|sp|Q41274|AGL8\_SINAL Agamous-like MADS box protein AGL8 homolog (MAI)  
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Identities = 66/81 (81%), Positives = 71/81 (87%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQEGQLVQCSNSSSVLLPQYCVTSSRDGFVERVGGENG 60  
K LQDHNN+LLKKIKEREK T QE QL+QCSN+SS+L PQYC+TSSRDGFV RV GEN  
Sbjct: 159 KVLQDHNNALLKKIKEREKNTVHQEVQLIQCSNNSILQPQYCLTSSRDGFVGRVEGENE 218

Query: 61 GASSLTEPNSLLPAWMLRPTT 81  
GASSL EPNSLLPAWMLRPTT  
Sbjct: 219 GASSLAEPNSLLPAWMLRPTT 239

☐ >gi|23304678|emb|CAD47852.1| MADS-box protein FUL-d [Brassica oleracea var. botrytis]  
Length = 242

Score = 121 bits (304), Expect = 2e-27  
Identities = 72/83 (86%), Positives = 76/83 (91%), Gaps = 2/83 (2%)

Query: 1 KALQDHNNSSLKKIKEREK--KTGQQEGQLVQCSNSSSVLLPQYCVTSSRDGFVERVGGE 58  
KALQDHNN+LLKKIKE+EK TGGQQEGQL+QCSN+SSVL PQYCVTSSRDG VERVGGE  
Sbjct: 159 KALQDHNNNTLLKKIKEKEKEKNTGQQEGQLIQCSNNSVLQPQYCVTSSRDGLVERVGGE 218

Query: 59 NGGASSLTEPNSLLPAWMLRPTT 81  
 NGG SSL EPNSLLPAWMLRPTT  
 Sbjct: 219 NGGTSSLIEPNSLLPAWMLRPTT 241

☐ >gi|23304676|emb|CAD47851.1| MADS-box protein FUL-c [Brassica oleracea var. boti  
 Length = 243

Score = 119 bits (299), Expect = 1e-26  
 Identities = 71/83 (85%), Positives = 75/83 (90%), Gaps = 2/83 (2%)

Query: 1 KALQDHNNSSLKKIKEREK--KTGQEGQLVQCSNSSSVLLPQYCVTSSRDGFVERVGGE 58  
 KALQDHNN+LLKKIKE+EK TKGQEGQL+QCSN+SSVL PQYCVTSSRDG VERVGGE  
 Sbjct: 159 KALQDHNNNTLLKKIKEKEKEKNTGQEGQLIQCSNNSVLPQYCVTSSRDGLVERVGGE 218

Query: 59 NGGASSLTEPNSLLPAWMLRPTT 81  
 NGGASSL PNSLLPAWMLRP T  
 Sbjct: 219 NGGASSLIGPNSLLPAWMLRPAT 241

☐ >gi|5070142|gb|AAD39036.1| MADS-box protein MADS1 [Nicotiana sylvestris]  
 Length = 245

Score = 47.4 bits (111), Expect = 6e-05  
 Identities = 36/84 (42%), Positives = 50/84 (59%), Gaps = 7/84 (8%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQ---EGQLVQCSNSSSVLLPQYCVTSSRDGFVERVGG 57  
 KALQ+ NN+L K++KEREK+ QQ E Q NSSS +L Q ++S G G  
 Sbjct: 159 KALQEQNNNLSKQVKEREKELAQQTQWEQQSHDLNSSFVLTQ-PLSSLHLGEAYPTAG 217

Query: 58 ENG---GASSLTEPNSLLPAWMLR 78  
 +NG G+S + N+++P WMLR  
 Sbjct: 218 DNGEVEGSSRQQQNTVMPPWMLR 241

☐ >gi|6606306|gb|AAF19164.1| floral binding protein 26 [Petunia x hybrida]  
 Length = 245

Score = 47.0 bits (110), Expect = 7e-05  
 Identities = 36/83 (43%), Positives = 47/83 (56%), Gaps = 6/83 (7%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQEGQLVQCS--NSSSVLLPQYCVTSSRDGFVERVGGE 58  
 KALQ+ NN L K++KEREK+ QQ Q NSSS +L Q + S G G+  
 Sbjct: 160 KALQEQNNKLSKQVKEREKELAQSQWEPQSHDLNSSFVLSQ-PLNSLHLGEAYPSAGD 218

Query: 59 NG---GASSLTEPNSLLPAWMLR 78  
 NG G+S PN+++P WMLR  
 Sbjct: 219 NGEVEGSSRQQPPNTVMPPWMLR 241

☐ >gi|32478069|gb|AAP83396.1| euFUL FRUITFULL-like MADS-box [Petunia x hybrida]  
 Length = 214

Score = 46.6 bits (109), Expect = 8e-05  
 Identities = 36/83 (43%), Positives = 47/83 (56%), Gaps = 6/83 (7%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQEGQLVQCS--NSSSVLLPQYCVTSSRDGFVERVGGE 58  
 KALQ+ NN L K++KEREK+ QQ Q NSSS +L Q + S G G+  
 Sbjct: 129 KALQEQNNKLSKQVKEREKELAQQSQWEPQSHDLNSSSFVLSQ-PLNSLHLGEAYPSAGD 187

Query: 59 NG---GASSLTEPNSLLPAWMLR 78  
 NG G+S PN+++P WMLR  
 Sbjct: 188 NGEVEGSSRQQPPNTVMPPWMLR 210

☐ >gi|27373049|gb|AAO12211.1| MADS11 [Nicotiana tabacum]  
 Length = 245

Score = 46.6 bits (109), Expect = 9e-05  
 Identities = 35/84 (41%), Positives = 49/84 (58%), Gaps = 7/84 (8%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQ---EGQLVQCSNSSSVLLPQYCVTSSRDGFVERVGG 57  
 KALQ+ NN L K++KEREK+ QQ E Q NSS+ +L Q ++S G G  
 Sbjct: 159 KALQEQNNKLSKQVKEREKELAQQTQWEQQSHDLNSSTFVLSQ-PLSSLHLGEAYSTAG 217

Query: 58 ENG---GASSLTEPNSLLPAWMLR 78  
 +NG G+S + N+++P WMLR  
 Sbjct: 218 DNGEVEGSSRQQQNTVMPPWMLR 241

☐ >gi|32478063|gb|AAP83393.1| euFUL FRUITFULL-like MADS-box [Pisum sativum]  
 Length = 199

Score = 45.1 bits (105), Expect = 3e-04  
 Identities = 35/78 (44%), Positives = 44/78 (56%), Gaps = 3/78 (3%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQEGQLVQCSNSSSVLLPQYCVTSSRDGFVERVGGENG 60  
 KALQ+ NN L KKIKE+EK Q E S+ L+PQ T + G + G+N  
 Sbjct: 124 KALQEKNNLLTKKIKEKEKALAQLELHNDMDLDSTALVPQPLETLNI-GCSPQDRGDNE 182

Query: 61 GASSLTEPNSLLPAWMLR 78  
 G S T+ N+LLP WMLR  
 Sbjct: 183 G--SQTQSNALLPHWMLR 198

☐ >gi|23428887|gb|AAM33098.1| TDR4 transcription factor [Lycopersicon esculentum]  
 Length = 245

Score = 43.9 bits (102), Expect = 6e-04  
 Identities = 34/86 (39%), Positives = 48/86 (55%), Gaps = 11/86 (12%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQEGQLVQCSNSSSVLLPQ-----YCVTSSRDGFVERV 55  
 +ALQ+ NN L KK+KEREK+ QQ + NSSS +LPQ + + + V  
 Sbjct: 159 RALQEQNNQLSKKVKEREKEVAQQNQWEI---NSSSFVLPQQLDSPHLGEAYQSTNVIDN 215

Query: 56 GGENGASSLTE---PNSLLPAWMLR 78  
 G GG+SS + N+++P WMLR  
 Sbjct: 216 GEVEGGSSSQQGAANNTVMPPQWMLR 241

☐ >gi|32478023|gb|AAP83373.1| FRUITFULL-like MADS-box [Heuchera americana]  
Length = 216

Score = 43.5 bits (101), Expect = 7e-04  
Identities = 39/90 (43%), Positives = 46/90 (51%), Gaps = 13/90 (14%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQ--QEGQLVQCSNSSSVLLP-----QYCVTSSRDG 50  
KALQ+ NN L KKIKE EK G+ Q Q Q SSS +L Q + D  
Sbjct: 126 KALQEQNNQLAKKIKENEKTVGENAQWQQPNQGHSTSSSFMLAPALPPPSLQLPSLNIGDT 185

Query: 51 FVERVGGENGASSLTEP--NSLLPAWMLR 78  
F R G NG A + T P N+L+P WMLR  
Sbjct: 186 FQAR-GVMNGDAGAQTRPSTNTLMPPWMLR 214

☐ >gi|4102111|gb|AAD01421.1| NAP1-1 [Nicotiana tabacum]  
Length = 245

Score = 43.1 bits (100), Expect = 0.001  
Identities = 34/84 (40%), Positives = 49/84 (58%), Gaps = 7/84 (8%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQ--EGQLVQCSNSSSVLLPQYCVTSSRDGFVERVGG 57  
+ALQ+ NN+L K++KE EK+ QQ E Q NSSS +L Q ++S G G  
Sbjct: 159 EALQEQNNNLKQVKKEGKELAQQTQWEQQSHDHLNSSFVLTQ-PLSSLHLGEAYPTAG 217

Query: 58 ENG---GASSLTEPNSLLPAWMLR 78  
+NG G+S + N+++P WMLR  
Sbjct: 218 DNGELEGSSRQQQNTVMPPWMLR 241

☐ >gi|4097509|gb|AAD09496.1| transcription factor NTSQUA4 [Nicotiana tabacum]  
Length = 186

Score = 42.7 bits (99), Expect = 0.001  
Identities = 34/84 (40%), Positives = 48/84 (57%), Gaps = 7/84 (8%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQ--EGQLVQCSNSSSVLLPQYCVTSSRDGFVERVGG 57  
KALQ+ NN L K++K REK+ QQ E Q NSS+ +L Q ++S G G  
Sbjct: 102 KALQEQNNKLSKQVKVREKELAQQTQWEQQSHDHLNSSFVLSQ-PLSSLHLGEAYSTAG 160

Query: 58 ENG---GASSLTEPNSLLPAWMLR 78  
+NG G+S + N+++P WMLR  
Sbjct: 161 DNGEVEGSSRQQQNTVMPPWMLR 184

☐ >gi|14518447|gb|AAF22139.2| MADS box protein [Capsicum annuum]  
Length = 247

Score = 42.4 bits (98), Expect = 0.002  
Identities = 36/86 (41%), Positives = 50/86 (58%), Gaps = 9/86 (10%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQ---EGQLVQCSNSSSVLLPQYCVTSSRDGFVERVG 56  
KALQ+ NN+L K++KEREK+ QQ E Q NSSS LP + ++ G V  
Sbjct: 159 KALQEQNNNLKQMKEREKQLAQHTPWEQQNHDLNSSFGLP-HPFNNNHLGEVYPTA 217

Query: 57 GENG---GASSLTEPN-SLLPAWMLR 78

G+NG G+S + N +++P WMLR  
 Sbjct: 218 GDNGEVEGSSRQQQNAAVMPPWMLR 243

☐ >gi|3913001|sp|Q42429|AGL8\_SOLTU Agamous-like MADS box protein AGL8 homolog (POT  
 gi|7446508|pir|T07100 MADS box protein homolog POTM1-1 - potato  
 gi|758565|gb|AAA92839.1| transcription factor  
 gi|758567|gb|AAA92840.1| transcription factor [Solanum tuberosum]  
 Length = 250

Score = 42.0 bits (97), Expect = 0.002  
 Identities = 34/88 (38%), Positives = 48/88 (54%), Gaps = 10/88 (11%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQE--GQLVQCSNSSSVLLPQ-----YCVTSSRDGFVE 53  
 +ALQ+ NN L KK+KEREK+ QQ Q NSS+ +LPQ + + ++ V  
 Sbjct: 159 RALQEQNNQLSKVKEREKEVAQQNQWDQQNHEINSSTFVLPQQLDSPHLGEAYQNTNVV 218

Query: 54 RVGGENGASSLTE---PNSLLPAWMLR 78  
 G GG SS + N+++P WMLR  
 Sbjct: 219 DNGEVEGGNSSQQQGAANNTVMPPQWMLR 246

☐ >gi|32478035|gb|AAP83379.1| euFUL FRUITFULL-like MADS-box [Lycopersicon esculent  
 Length = 209

Score = 41.6 bits (96), Expect = 0.003  
 Identities = 33/85 (38%), Positives = 47/85 (55%), Gaps = 11/85 (12%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQEGQLVQCSNSSSVLLPQ-----YCVTSSRDGFVERV 55  
 +ALQ+ NN L KK+KEREK+ QQ + NSSS +LPQ + + + V  
 Sbjct: 128 RALQEQNNQLSKVKEREKEVAQQNQWEI---NSSSFVLPQQLDSPHLGEAYQSTNVIDN 184

Query: 56 GGENGASSLTE---PNSLLPAWML 77  
 G GG+SS + N+++P WML  
 Sbjct: 185 GEVEGGSSSQQGAANNTVMPPWML 209

☐ >gi|4097511|gb|AAD09497.1| transcription factor NTSQUA12 [Nicotiana tabacum]  
 Length = 186

Score = 41.6 bits (96), Expect = 0.003  
 Identities = 34/84 (40%), Positives = 48/84 (57%), Gaps = 7/84 (8%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQ--EGQLVQCSNSSSVLLPQYCVTSSRDGFVERVGG 57  
 KALQ+ NN+L K++K REK+ QQ E Q NS S +L Q ++S G G  
 Sbjct: 102 KALQEQNNNLSKQVKVREKELAQQTQWEQQSHDLNPSFVLTQ-PLSSLHLGEAYPTAG 160

Query: 58 ENG---GASSLTEPNSLLPAWMLR 78  
 +NG G+S + N+++P WMLR  
 Sbjct: 161 DNGEVEGSSRQQQNTVMPPWMLR 184

☐ >gi|3912987|sp|O22328|AGL8\_SOLCO Agamous-like MADS box protein AGL8 homolog  
 gi|7446507|pir|T07902 MADS box protein - Commerson's wild potato  
 gi|2290778|gb|AAB65161.1| MADS box transcription factor [Solanum commersonii]

Length = 250

Score = 41.6 bits (96), Expect = 0.003

Identities = 34/88 (38%), Positives = 49/88 (55%), Gaps = 10/88 (11%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQEE--GQLVQCSNSSSVLLPQ-----YCVTSSRDGFVE 53  
 +ALQ+ NN L KK+KEREK+ QQ Q NSS+ +LPQ + +S++ V  
 Sbjct: 159 RALQEQNNQLSKKVKEREKEVEQQNQWDQONHEINSSTFVLPQQLDSPHLGEASQNTNVV 218

Query: 54 RVGGENGGASSLTE---PNSLLPAWMLR 78  
 G GG SS + N+++P WM+R  
 Sbjct: 219 DNGEVEGGNSSQXQGAANNTVMPQWMVR 246

☐ >gi|6634708|gb|AAF19721.1| MADS box transcription factor [Petunia x hybrida]  
 Length = 246

Score = 40.8 bits (94), Expect = 0.006

Identities = 32/85 (37%), Positives = 48/85 (56%), Gaps = 8/85 (9%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQ-----QEGQLVQCSNSSSVLLPQYCVTSSRDGFVERV 55  
 K+LQ+ NN L KK+KEREK+ Q Q+ + ++SSS +LPQ + S G +  
 Sbjct: 159 KSLQEQNNLLSKKVKEREKELAQQTQWEQQNNHHEINSSSSSFVLPQ-PLDSPHLGEAYQS 217

Query: 56 GGENG--GASSLTEPNSLLPAWMLR 78  
 +NG +S +P + +P WMLR  
 Sbjct: 218 TVDNGEVEGASQQQPANTMPPWMLR 242

☐ >gi|10946429|gb|AAG24909.1| MADS-box protein EAP1 [Eucalyptus globulus]  
 Length = 244

Score = 40.4 bits (93), Expect = 0.006

Identities = 32/81 (39%), Positives = 47/81 (58%), Gaps = 7/81 (8%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQEGQLVQCSNS--SSVLLPQYCVTSSRDG-FVERVGG 57  
 +ALQ+ NN L KKIKE+E+ QQ Q Q ++ S V+LP Y + +G + R G  
 Sbjct: 159 RALQEQNNLLTKKIKEKERALAQQ-AQWEQQDHALDSPVVLPHYLPPLDINGSYQARHNG 217

Query: 58 ENGGASSLTEP--NSLLPAWM 76  
 + G +LT+P +LLP W+  
 Sbjct: 218 HDDG-ENLTQPRAGTLLPPWI 237

☐ >gi|3947985|gb|AAC83170.1| MADS-box protein 2 [Malus x domestica]  
 Length = 255

Score = 38.9 bits (89), Expect = 0.019

Identities = 34/93 (36%), Positives = 42/93 (45%), Gaps = 15/93 (16%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQ---EGQLVQCSNSSSVLLPQ-----YCVT 45  
 KALQ+ NN L KK+KE+E QQ E Q NSSS LLP+ Y  
 Sbjct: 159 KALQEQNNLLAKKVKENAVAAQQAQLEHVQEQRNLSSSSLLPRALQSLNFGSGSNYQAI 218

Query: 46 SSRDGFVERVGGENGGASSLTEPNSLLPAWMLR 78  
 S +G + PN LLPAW++R

Sbjct: 219 RSSEGIPGDNQQYGDDETPTPHRPNMLLPWIVR 251

☐ >gi|33342030|dbj|BAC80249.1| MADS-box transcription factor [Houttuynia cordata]  
Length = 245

Score = 38.5 bits (88), Expect = 0.026

Identities = 30/83 (36%), Positives = 40/83 (48%), Gaps = 5/83 (6%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQEGQLVQCSNSSSV-LLPQYCVTSSRDGFVERVGG-- 57

KALQ+ NN L KK++E++K QQ Q N +S L + + G + G

Sbjct: 159 KALQEQNNMLEKKVQEKQKAKAQQTRWENQSQNQNSAPFLFSLPLPNLNMGTYHQENGTE 218

Query: 58 --ENGGASSLTEPNSLLPAWMLR 78

E A L NS +PAWMLR

Sbjct: 219 IREQEAAARPLAHSNSQMPAWMLR 241

☐ >gi|32478037|gb|AAP83380.1| euFUL FRUITFULL-like MADS-box [Lycopersicon esculent]  
Length = 210

Score = 37.4 bits (85), Expect = 0.052

Identities = 23/44 (52%), Positives = 29/44 (65%), Gaps = 3/44 (6%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQ---EGQLVQCSNSSSVLLPQ 41

KALQ+ NN+L K++KEREK+ QQ E Q NSSS +LP

Sbjct: 126 KALQEQNNNLSKQVKEREKEMAQQTPWEQQSHDHLNSSSFVLP 169

☐ >gi|32478019|gb|AAP83371.1| euFUL FRUITFULL-like MADS-box [Corylopsis sinensis]  
Length = 229

Score = 37.0 bits (84), Expect = 0.071

Identities = 29/79 (36%), Positives = 38/79 (48%), Gaps = 2/79 (2%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQ--QEGQLVQCSNSSSVLLPQYCVTSSRDGFVERVGGE 58

K+LQ+ NNSL KKIKE+E Q Q Q NS +LL Q + + +

Sbjct: 148 KSLQEENNSLSKKIKEKENALAHRAQWEQQNQGLNSFPILLSQPPQSLNIGTYQTGCSEG 207

Query: 59 NGGASSLTEPNSLLPAWML 77

G PN+LLP WM+

Sbjct: 208 EEGTPFQQRPNNTLLPHWMV 226

☐ >gi|31979209|gb|AAP68794.1| MADS-box protein [Acacia mangium]  
Length = 206

Score = 36.2 bits (82), Expect = 0.12

Identities = 29/85 (34%), Positives = 44/85 (51%), Gaps = 6/85 (7%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQEGQLVQCSNSSSVLLPQYCVTSSRDGFVERVGG--E 58

K LQ+ NN L K+IKE+EK ++ + + N L+ S+ VE GG +

Sbjct: 123 KKLQEQNNLLAKEIKEKEKALAEKARE--EKHNDEDALVQPQLPPSNIGEIVEARGGAED 180

Query: 59 NGGASSLTEPNS--LLPAWMLRPTT 81

N ++ +P S LLP+WML P +  
 Sbjct: 181 NEATTTTHHQPRSGPLLPSWMLPPIS 205

☐ >gi|5070140|gb|AAD39035.1| MADS-box protein MADS5 [Nicotiana tabacum]  
 Length = 242

Score = 35.0 bits (79), Expect = 0.26  
 Identities = 23/47 (48%), Positives = 30/47 (63%), Gaps = 3/47 (6%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQE--GQLVQCSNSSSVLL-PQYCV 44  
 KA+Q+ NN L KKIKE++K G+Q Q Q NS+S LL P C+  
 Sbjct: 161 KAIQEENMMLSKKIKEKDKTVGKQAEWHQQNQVPNSASFLLQPHPC 207

☐ >gi|32478045|gb|AAP83384.1| euAP1 APETALA1-like MADS-box [Phytolacca americana]  
 Length = 239

Score = 35.0 bits (79), Expect = 0.32  
 Identities = 23/65 (35%), Positives = 37/65 (56%), Gaps = 7/65 (10%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQEG-----QLVQCSNSSSVLLPQYCVT--SSRDGFVE 53  
 KA+Q+ NN L+KKIKEREK + +G Q + +S+ LLP + ++ D +  
 Sbjct: 154 KAMQEQQNNMLVKKIKEREKAMAEAQGMQWQRQQNEPPEASNFLPPPLTSWNTAGDAYHG 213

Query: 54 RVGGE 58  
 ++ GE  
 Sbjct: 214 QIAGE 218

☐ >gi|13384068|gb|AAK21258.1| MADS-box transcription factor FBP29 [Petunia x hybr]  
 Length = 245

Score = 35.0 bits (79), Expect = 0.32  
 Identities = 26/83 (31%), Positives = 42/83 (50%), Gaps = 7/83 (8%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQEGQLVQCSNSSSVLLPQYCVTSSRDGFVERVGGENG 60  
 +ALQ+ NN + KK+KE E KT + Q + N ++ ++PQ S + +GG G  
 Sbjct: 159 RALQEQQNNLMTKKLKENE-KTQSGQTQPISSQNDATFMVPQPPSLSHHVANLT-IGGAFG 216

Query: 61 GAS-----SLTEPNSLLPAWMLR 78  
 + + NS +P WM+R  
 Sbjct: 217 AKTVTNTNGVQASNSQMPPWMIR 239

☐ >gi|32478003|gb|AAP83363.1| euFUL FRUITFULL-like MADS-box [Antirrhinum majus]  
 Length = 212

Score = 33.9 bits (76), Expect = 0.71  
 Identities = 33/89 (37%), Positives = 40/89 (44%), Gaps = 16/89 (17%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQ----QEGQLVQCSNSSSVLLPQYC-----VTSSR 48  
 KALQ+ NN L KKIKE++ + Q+ Q SS+ PQ R  
 Sbjct: 128 KALQEQQNNLLAKKIKEREQEFA RTNQWQQHQNHNFTSSTAGAPQSLSSLSEICQGQR 187



Query: 49 DGFVERVGGENGASSLTEPNSLLPAWML 77  
 D E G N SS N +LP WML  
 Sbjct: 188 DNNGEVEGSRNQSS---NKILPPWML 212

☐ >gi|34911244|ref|NP\_916969.1| P0445E10.20 [Oryza sativa (japonica cultivar-group)]  
 gi|24636779|dbj|BAB86060.2| P0445E10.20 [Oryza sativa (japonica cultivar-group)]  
 Length = 1130

Score = 33.1 bits (74), Expect = 1.1  
 Identities = 17/49 (34%), Positives = 28/49 (57%), Gaps = 2/49 (4%)

Query: 34 SSSVLLPQYCVTSSRDGFVERVGGENGASSLTE-PNSLLPAWMLRPTT 81  
 + + L P C +R VE + G+NGG S + P++ PAW+ RP++  
 Sbjct: 18 APATLAPCPCHRGTR-AVVEVLTGQNGGTSHTSAAPHTTAPAWLARPS 65

☐ >gi|20805023|dbj|BAB92698.1| P0478H03.14 [Oryza sativa (japonica cultivar-group)]  
 Length = 1171

Score = 33.1 bits (74), Expect = 1.2  
 Identities = 17/49 (34%), Positives = 28/49 (57%), Gaps = 2/49 (4%)

Query: 34 SSSVLLPQYCVTSSRDGFVERVGGENGASSLTE-PNSLLPAWMLRPTT 81  
 + + L P C +R VE + G+NGG S + P++ PAW+ RP++  
 Sbjct: 18 APATLAPCPCHRGTR-AVVEVLTGQNGGTSHTSAAPHTTAPAWLARPS 65

☐ >gi|32478049|gb|AAP83386.1| FRUITFULL-like MADS-box [Phytolacca americana]  
 Length = 212

Score = 32.7 bits (73), Expect = 1.4  
 Identities = 26/85 (30%), Positives = 42/85 (49%), Gaps = 7/85 (8%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQE---GQLVQCSNSSSVLLPQYCVTSS---RDGFVE 53  
 KA+Q+ NN L+K +KE+ K +E Q + S+S+ + P + S + VE  
 Sbjct: 126 KAMQEQNNLLVKLVEKGTQVIEENPSQALMLSSSNPLSFPSLSIGGSYQERTEMGVE 185

Query: 54 RVGGENGASSLTEPNSLLPAWMLR 78  
 +V + G N+ +P WMLR  
 Sbjct: 186 QVHYQGQGQVPPNSNTTTPPWMLR 210

☐ >gi|32478115|gb|AAP83419.1| euAP1 APETALA1-like MADS-box [Paeonia suffruticosa]  
 Length = 226

Score = 32.7 bits (73), Expect = 1.4  
 Identities = 20/49 (40%), Positives = 31/49 (63%), Gaps = 3/49 (6%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQ---EGQLVQCSNSSSVLLPQYCVTS 46  
 +A+Q+ NN L K+IKE+EK QQ E Q+ N+S+ LL + +T+  
 Sbjct: 142 RAIQEQNNLLAKQIKEKEKTMAQQAQWEQIIHGPNASAYLLSPHELTT 190

☐ >gi|22091473|emb|CAC81068.1| MADS box transcription factor [Daucus carota subsp.  
Length = 242

Score = 32.3 bits (72), Expect = 1.7  
Identities = 21/43 (48%), Positives = 25/43 (58%), Gaps = 2/43 (4%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQEGQLVQ--CSNSSSVLLPQ 41  
KA+Q+ N L KIKEREK QQ Q N S+ L+PQ  
Sbjct: 159 KAIQEENGKLTKKIKEREKTMVQQAQWEKQNPSPNLSTFLMPQ 201

☐ >gi|16874557|gb|AAK72467.1| MADS-box transcription factor DEFH28 [Antirrhinum m  
Length = 252

Score = 32.3 bits (72), Expect = 1.8  
Identities = 29/91 (31%), Positives = 48/91 (52%), Gaps = 14/91 (15%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQEGQL---VQCSNSSSVLLPQ-----YCVTSSR 48  
++LQD NN L KIK+ EK+ +++ + Q S+S ++LL C+ S  
Sbjct: 159 RSLQDQNNILAKKIKDNEKQNEKQQDVHEGFAQSSSSINMLLQPPATQLHAVPCLPIS- 217

Query: 49 DGFVERVGGENG-ASSLTEPNSLLPAWMLR 78  
GF + V E GG + + + S +P W+L+  
Sbjct: 218 GGFQQTVRVEEGDRTRIADSRSHIPPWLLQ 248

☐ >gi|4102113|gb|AAD01422.1| NAP1-2 [Nicotiana tabacum]  
Length = 242

Score = 32.3 bits (72), Expect = 2.0  
Identities = 22/47 (46%), Positives = 28/47 (59%), Gaps = 3/47 (6%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQE--GQLVQCSNSSSVLL-PQYCV 44  
KA+Q+ NN L KIK+ GQQ Q Q S+S LL P C+  
Sbjct: 161 KAIQEENMLSKKIKEKDNTVGQQVEWHQQNQVPTSTSFLLQPHPCL 207

☐ >gi|5070144|gb|AAD39037.1| MADS-box protein MADS2 [Nicotiana sylvestris]  
Length = 242

Score = 32.0 bits (71), Expect = 2.5  
Identities = 22/47 (46%), Positives = 28/47 (59%), Gaps = 3/47 (6%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQE--GQLVQCSNSSSVLL-PQYCV 44  
KA+Q+ NN L KIK+ GQQ Q Q S+S LL P C+  
Sbjct: 161 KAIQEENMLSKKIKEKDNTVGQQVEWHQQNQVPTSASFLLQPHPCL 207

☐ >gi|1483228|emb|CAA67967.1| MADS3 protein [Betula pendula]  
Length = 243

Score = 32.0 bits (71), Expect = 2.7  
Identities = 23/45 (51%), Positives = 26/45 (57%), Gaps = 4/45 (8%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQ---EGQLVQCSN-SSSVLLPQ 41  
 KA+Q+ N L KKIKE+EK Q E Q N SSS LLPQ  
 Sbjct: 159 KAIQEQTILAKKIKEKEKTVAQHVDWEQQNQGAPNGSSSFLLPQ 203

☐ >gi|1483232|emb|CAA67969.1| MADS5 protein [Betula pendula]  
 Length = 244

Score = 32.0 bits (71), Expect = 2.8  
 Identities = 37/83 (44%), Positives = 45/83 (54%), Gaps = 6/83 (7%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQEGQLVQCSNSSSV--LLPQYCVTSSRDGFVERVGG 58  
 KALQ+ NN L KK+KE+EK+ QQ Q SV LLPQ +S G ++ G  
 Sbjct: 159 KALQEQNNVLAKKVKEKEKELAQQAQWEQQSHTLDSVPSLLPQPLQSSLNIGGSQQARG- 217

Query: 59 NGGASSLTEP---NSLLPAWMLR 78  
 NG T P N+LLP WMLR  
 Sbjct: 218 NGRVDEGTPPHRANALLPPWMLR 240

☐ >gi|3912999|sp|Q40170|AGL8\_LYCES Agamous-like MADS box protein AGL8 homolog (TM4  
 gi|542035|pir|S23730 MADS box protein TDR4 - tomato  
 gi|19382|emb|CAA43169.1| TDR4 [Lycopersicon esculentum]  
 Length = 227

Score = 31.6 bits (70), Expect = 3.0  
 Identities = 15/26 (57%), Positives = 18/26 (69%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQEG 26  
 +ALQ+ NN L KK+KEREK Q G  
 Sbjct: 159 RALQEQNNQLSKKVKEREKSAQQISG 184

☐ >gi|27804357|gb|AAO22980.1| MADS-box transcription factor CDM41 [Chrysanthemum ]  
 Length = 243

Score = 31.6 bits (70), Expect = 3.3  
 Identities = 25/81 (30%), Positives = 38/81 (46%), Gaps = 3/81 (3%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQEGQL-VQCSNSSSVLLPQYCVTS--SRDGFVERVGG 57  
 K LQ+ NNSL KK+KE EK + QQ ++ + Y V S + F+  
 Sbjct: 159 KTLQERNNSLSKKLKENEKNSEQQNERVELPQPPPPPPQPYPYVPSFATSRPFIGAAMR 218

Query: 58 ENGGASSLTEPNSLLPAWMLR 78  
 E A + +++P WM+R  
 Sbjct: 219 EEELARAHVSTTMMPLWMIR 239

☐ >gi|32478065|gb|AAP83394.1| FRUITFULL-like MADS-box [Petunia x hybrida]  
 Length = 213

Score = 31.2 bits (69), Expect = 4.0  
 Identities = 28/83 (33%), Positives = 38/83 (45%), Gaps = 6/83 (7%)

Query: 1 KALQDHNNSSLKKIKEREKKTG-----QQEGQLVQCSNSSSVLLPQYCVTSSRDGFVERV 55

+ALQ+ NN L KK+K+ EK +Q+ PQ + S G ++  
 Sbjct: 128 RALQEQNNLLAKKLKDNKTVARPPQLEQQNLPHNTPTFMFPPPPQSLHSLTIGGNFQI 187  
 Query: 56 GGENGGASSLTEPNSLLPAWMLR 78  
 G EN GA N L+P WMLR  
 Sbjct: 188 GQEN-GAQIRPNSNPLMPPWMLR 209

☐ >gi|32478017|gb|AAP83370.1| euAP1 APETALA1-like MADS-box [Corylopsis sinensis]  
 Length = 218

Score = 31.2 bits (69), Expect = 4.1  
 Identities = 15/24 (62%), Positives = 18/24 (75%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQ 24  
 KA+Q+ NN L KKIKE+EK QQ  
 Sbjct: 133 KAMQEQNNMLAKKIKEKEKTMTQQ 156

☐ >gi|1483230|emb|CAA67968.1| MADS4 protein [Betula pendula]  
 Length = 260

Score = 30.4 bits (67), Expect = 6.9  
 Identities = 31/98 (31%), Positives = 39/98 (39%), Gaps = 22/98 (22%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQEGQLVQCS---NSSSVLLPQYCVTSSRDG----- 50  
 KALQ+ NN L KKIKE EK + L Q S N S+ +L +  
 Sbjct: 159 KALQEQNNLLSKKIKENEKAVAEH-AHLEQPSIGQNLSTFMLSPLQQPQPQPQLQPQPPT 217  
 Query: 51 -----FVERVGGENGASSLTEPNSLLPAWML 77  
 F G E+ GA + N L+P WML  
 Sbjct: 218 LPLPSLTIGGTFAQAGDEDAGAQTRPSANRLMPPWML 255

☐ >gi|16549085|dbj|BAB70749.1| putative MADS-domain transcription factor MpMADS15  
 praecocissima]  
 Length = 240

Score = 30.4 bits (67), Expect = 6.9  
 Identities = 28/80 (35%), Positives = 39/80 (48%), Gaps = 2/80 (2%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQQEGQLVQCSN---VLLPQYCVTSSRDGFVERVGGE 58  
 K+L++ NN L K+I+E+EK QQ Q + SS L T + + + E  
 Sbjct: 157 KSLREQNNMLEKEIQEKEKAMAQQAQWEQQNQSSSHPSWLASPLPTLNIGTYHQGNEVE 216  
 Query: 59 NGGASSLTEPNSLLPAWMLR 78  
 GA NSL+P WMLR  
 Sbjct: 217 EEGARPPARTNSLMPPWMLR 236

☐ >gi|34910342|ref|NP\_916518.1| P0684B02.5 [Oryza sativa (japonica cultivar-group)]  
 gi|34911552|ref|NP\_917123.1| P0421H07.25 [Oryza sativa (japonica cultivar-group)]  
 gi|13872912|dbj|BAB44018.1| P0684B02.5 [Oryza sativa (japonica cultivar-group)]  
 gi|20804606|dbj|BAB92297.1| P0421H07.25 [Oryza sativa (japonica cultivar-group)]  
 Length = 326

Score = 30.4 bits (67), Expect = 7.3  
 Identities = 18/49 (36%), Positives = 27/49 (55%), Gaps = 2/49 (4%)

Query: 34 SSSVLLPQYCVTSSRDGFVERVGGENGASSL-TEPNSLLPAWMLRPTT 81  
 + + L P C +R VE + G+NGGAS P + PAW+ RP++  
 Sbjct: 22 APATLAPCPCHRGR-ATVEVLGTQNGGASHTGAAPPTTAPAWLARPS 69

☐ >gi|32478013|gb|AAP83368.1| FRUITFULL-like MADS-box [Chelidonium majus]  
 Length = 217

Score = 30.0 bits (66), Expect = 8.2  
 Identities = 29/91 (31%), Positives = 37/91 (40%), Gaps = 18/91 (19%)

Query: 1 KALQDHNNSSLKKIKEREKKTGQEGQLVQCSNSSSVL-----LPQYCVTS 46  
 KAL + N L KKIK++E++ Q Q NSSS L LP + +  
 Sbjct: 131 KALHEQNILLGKKIKQKEEQIAQWSAQQNDAAQNSSSFLTQAPQNSQSFLTQALPSLTLRT 190

Query: 47 SRDGFVERVGGENGASSLTEPNSLLPAWML 77  
 V E GA S N +P WML  
 Sbjct: 191 GYYQTARVVVCEEDGARS---NMXMPPWML 217

☐ >gi|20219014|gb|AAM15774.1| MADS-box transcription factor MADS-MC [Lycopersicon]  
 Length = 244

Score = 30.0 bits (66), Expect = 8.9  
 Identities = 20/48 (41%), Positives = 29/48 (60%), Gaps = 4/48 (8%)

Query: 1 KALQDHNNSSLKKIKEREK---KTGQEGQLVQCSNSSSVLL-PQYCV 44  
 +A+ + NN L KKIKE++K + G+ Q Q S S+S LL P C+  
 Sbjct: 161 RAILEENNMLTKKIKEKDKIVEQQGEWHQQTNQVSTSTSFLQLPHQCL 208




Database: All non-redundant GenBank CDS  
 translations+PDB+SwissProt+PIR+PRF  
 Posted date: Dec 18, 2003 12:38 AM  
 Number of letters in database: 517,909,209  
 Number of sequences in database: 1,580,593

Lambda K H  
 0.307 0.126 0.353

Gapped  
 Lambda K H  
 0.267 0.0410 0.140

Matrix: BLOSUM62  
 Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 22,065,571  
Number of Sequences: 1580593  
Number of extensions: 741937  
Number of successful extensions: 1820  
Number of sequences better than 10.0: 23  
Number of HSP's better than 10.0 without gapping: 16  
Number of HSP's successfully gapped in prelim test: 7  
Number of HSP's that attempted gapping in prelim test: 1795  
Number of HSP's gapped (non-prelim): 24  
length of query: 84  
length of database: 517,909,209  
effective HSP length: 60  
effective length of query: 24  
effective length of database: 423,073,629  
effective search space: 10153767096  
effective search space used: 10153767096  
T: 11  
A: 40  
X1: 16 ( 7.1 bits)  
X2: 38 (14.6 bits)  
X3: 64 (24.7 bits)  
S1: 42 (21.6 bits)  
S2: 66 (30.0 bits)



## results of BLAST

**BLASTP 2.2.6 [Apr-09-2003]**

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1071780642-16793-145283596418.BLASTQ4

**Query=**

(34 letters)

**Database:** All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PRF

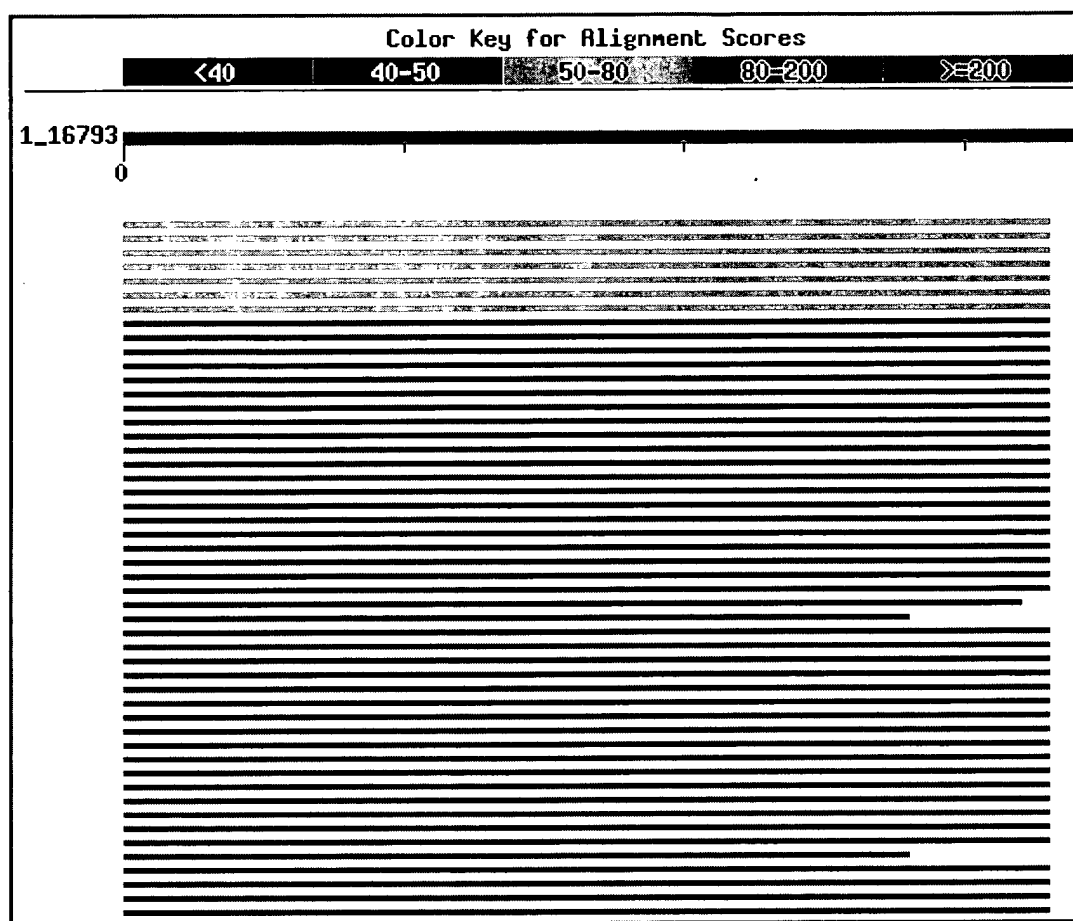
1,580,593 sequences; 517,909,209 total letters

If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

### Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:				Score (bits)	E Value
gi 18424410 ref NP_568929.1	MADS-box protein [Arabidopsis ...	69	2e-11		
gi 23304674 emb CAD47850.1	MADS-box protein FUL-b [Brassic...	69	3e-11		
gi 3913000 sp Q41274 AGL8_SINAL	Agamous-like MADS box prote...	68	5e-11		
gi 23304676 emb CAD47851.1	MADS-box protein FUL-c [Brassic...	65	3e-10		
gi 23304678 emb CAD47852.1	MADS-box protein FUL-d [Brassic...	65	3e-10		
gi 23304672 emb CAD47849.1	MADS-box protein FUL-a [Brassic...	65	3e-10		
gi 1483232 emb CAA67969.1	MADS5 protein [Betula pendula]	50	8e-06		
gi 13446154 emb CAC35027.1	MADS-box transcription factor [...	47	1e-04		
gi 32478063 gb AAP83393.1	euFUL FRUITFULL-like MADS-box [P...	46	2e-04		
gi 16162 emb CAA78909.1	AP1 [Arabidopsis thaliana]	45	3e-04		
gi 28381535 gb AAF12699.2	PTM1 [Populus tremuloides]	45	3e-04		
gi 14518447 gb AAF22139.2	MADS box protein [Capsicum annuum]	45	3e-04		
gi 15222220 ref NP_177074.1	floral homeotic gene APETALA1 ...	45	3e-04		
gi 20799348 gb AAM28451.1	apetala 1 [Arabidopsis thaliana]	45	4e-04		
gi 6634708 gb AAF19721.1	MADS box transcription factor [Pe...	45	4e-04		
gi 3646320 emb CAA04321.1	MADS-box protein [Malus x domest...	45	4e-04		
gi 32478021 gb AAP83372.1	euAP1 APETALA1-like MADS-box [He...	45	4e-04		
gi 20799358 gb AAM28456.1	apetala 1 [Arabidopsis thaliana]	45	4e-04		
gi 20799344 gb AAM28449.1	apetala 1 [Arabidopsis thaliana]	45	4e-04		
gi 20799346 gb AAM28450.1	apetala 1 [Arabidopsis thaliana]	45	5e-04		
gi 20799340 gb AAM28447.1	apetala 1 [Arabidopsis thaliana]...	45	5e-04		
gi 20799362 gb AAM28458.1	apetala 1 [Arabidopsis thaliana]	45	5e-04		
gi 20799364 gb AAM28459.1	apetala 1 [Arabidopsis thaliana]	45	5e-04		



gi 27657753 gb AAO18232.1	MADS-box transcriptional factor ...	44	5e-04
gi 21593537 gb AAM65504.1	homeotic protein boi1AP1, putati...	44	5e-04
gi 32478037 gb AAP83380.1	euFUL FRUITFULL-like MADS-box [L...	44	5e-04
gi 602906 emb CAA56658.1	SLM4 [Silene latifolia]	44	5e-04
gi 32478017 gb AAP83370.1	euAP1 APETALA1-like MADS-box [Co...	44	6e-04
gi 4416347 gb AAD20329.1	MADS C-2 protein; MADS-box protei...	44	6e-04
gi 82313 pir S20886	MADS box protein squa - garden snapdra...	44	7e-04
gi 1561780 gb AAB08876.1	homeotic protein boi2AP1 [Brassic...	44	7e-04
gi 32478023 gb AAP83373.1	FRUITFULL-like MADS-box [Heucher...	44	8e-04
gi 1561778 gb AAB08875.1	homeotic protein boi1AP1 [Brassic...	44	8e-04
gi 28381537 gb AAF12700.2	PTM2 [Populus tremuloides]	44	8e-04
gi 4102111 gb AAD01421.1	NAP1-1 [Nicotiana tabacum]	44	9e-04
gi 32478045 gb AAP83384.1	euAP1 APETALA1-like MADS-box [Ph...	44	9e-04
gi 6707086 gb AAF25589.1	apetalal [Arabidopsis lyrata] >gi...	44	0.001
gi 29372764 emb CAD23417.1	m4 [Zea mays]	44	0.001
gi 3913047 sp Q41276 AP1 SINAL	Floral homeotic protein APET...	44	0.001
gi 3947985 gb AAC83170.1	MADS-box protein 2 [Malus x domes...	44	0.001
gi 32478095 gb AAP83409.1	euAP1 APETALA1-like MADS-box [Sy...	43	0.001
gi 3912987 sp O22328 AGL8 SOLCO	Agamous-like MADS box prote...	43	0.001
gi 602908 emb CAA56659.1	SLM5 [Silene latifolia]	43	0.001
gi 5070142 gb AAD39036.1	MADS-box protein MADS1 [Nicotiana...	43	0.001
gi 27804355 gb AAO22979.1	MADS-box transcription factor CD...	43	0.001
gi 27373049 gb AAO12211.1	MADS11 [Nicotiana tabacum]	43	0.002
gi 30580167 sp Q39081 CAL ARATH	Transcription factor CAULIF...	42	0.002
gi 27542946 gb AAO16552.1	apetala 1-like protein [Metrosid...	42	0.002
gi 11120557 gb AAG30923.1	MADS box protein AP2L [Eucalyptu...	42	0.002
gi 22091473 emb CAC81068.1	MADS box transcription factor [...]	42	0.002
gi 23428887 gb AAM33098.1	TDR4 transcription factor [Lycop...	42	0.002
gi 887392 emb CAA86024.1	BOAP1 [Brassica oleracea]	42	0.003
gi 3688589 dbj BAA33457.1	MADS box transcription factor [T...	42	0.003
gi 3912999 sp Q40170 AGL8 LYCES	Agamous-like MADS box prote...	42	0.003
gi 32478035 gb AAP83379.1	euFUL FRUITFULL-like MADS-box [L...	42	0.003
gi 32478089 gb AAP83406.1	FRUITFULL-like MADS-box [Ranuncu...	42	0.003
gi 10946429 gb AAG24909.1	MADS-box protein EAP1 [Eucalyptu...	42	0.003
gi 29372748 emb CAD23408.1	putative MADS-domain transcript...	42	0.003
gi 18996775 gb AAL83209.1	MADS-box transcription factor HA...	42	0.003
gi 30090030 gb AAO72630.1	MADS box transcription factor AP...	42	0.003
gi 4097511 gb AAD09497.1	transcription factor NTSQUA12 [Ni...	42	0.003
gi 31979209 gb AAP68794.1	MADS-box protein [Acacia mangium]	42	0.003
gi 32478025 gb AAP83374.1	euFUL FRUITFULL-like MADS-box [H...	42	0.004
gi 30721847 gb AAP33790.1	MADS-box protein TaVRT-1 [Tritic...	42	0.004
gi 31712055 gb AAP68361.1	putative MADS box protein [Oryza...	42	0.004
gi 6606306 gb AAF19164.1	floral binding protein 26 [Petuni...	41	0.004
gi 12019658 gb AAF66997.2	FDRMADS6 [Oryza sativa]	41	0.004
gi 32478069 gb AAP83396.1	euFUL FRUITFULL-like MADS-box [P...	41	0.004
gi 21070923 gb AAM34398.1	AP1-like MADS-box protein [Oryza...	41	0.005
gi 30526323 gb AAP32475.1	MADS-box protein 6 [Vitis vinifera]	41	0.005
gi 4204232 gb AAD10625.1	MADS-box protein 1 [Lolium temule...	41	0.005
gi 7592642 dbj BAA94342.1	AP1-like MADS box protein [Oryza...	41	0.005
gi 28630953 gb AAO45873.1	MADS1 [Lolium perenne]	41	0.006
gi 4097509 gb AAD09496.1	transcription factor NTSQUA4 [Nic...	41	0.006
gi 6606070 gb AAF19047.1	MADS14 protein [Oryza sativa]	41	0.006
gi 9367309 emb CAB97352.1	MADS-box protein 5 [Hordeum vulg...	41	0.006
gi 32478015 gb AAP83369.1	FRUITFULL-like MADS-box [Chelido...	41	0.006
gi 4102113 gb AAD01422.1	NAP1-2 [Nicotiana tabacum]	40	0.008
gi 3913001 sp Q42429 AGL8 SOLTU	Agamous-like MADS box prote...	40	0.008
gi 32478077 gb AAP83400.1	FRUITFULL-like MADS-box [Papaver...	40	0.009
gi 13384068 gb AAK21258.1	MADS-box transcription factor FB...	40	0.009
gi 1483228 emb CAA67967.1	MADS3 protein [Betula pendula]	40	0.009
gi 642589 gb AAA64789.1	amino acid feature: K-box, bp 283....	40	0.009

gi 5070140 gb AAD39035.1	MADS-box protein MADS5 [Nicotiana...	40	0.010
gi 5070144 gb AAD39037.1	MADS-box protein MADS2 [Nicotiana...	40	0.010
gi 32478109 gb AAP83416.1	FRUITFULL-like MADS-box [Tradesc...	40	0.011
gi 11037010 gb AAG27459.1	MADS-box protein EAP2S [Eucalypt...	40	0.011
gi 4097513 gb AAD09498.1	transcription factor NTSQUA15 [Ni...	40	0.012
gi 18395839 ref NP_564243.1	floral regulatory gene CAULIFL...	40	0.012
gi 16874557 gb AAK72467.1	MADS-box transcription factor DE...	40	0.013
gi 32478065 gb AAP83394.1	FRUITFULL-like MADS-box [Petunia...	40	0.016
gi 6469345 emb CAB61825.1	DNA-binding protein [Brassica ra...	40	0.016
gi 32452882 emb CAC86183.1	MADS box protein [Malus x domes...	39	0.020
gi 28630955 gb AAO45874.1	MADS2 [Lolium perenne]	39	0.020
gi 6010661 gb AAF01210.1	squamosa/apetalal1 homolog [Actini...	39	0.021
gi 4204234 gb AAD10626.1	MADS-box protein 2 [Lolium temule...	39	0.023
gi 1483230 emb CAA67968.1	MADS4 protein [Betula pendula]	39	0.025
gi 32478051 gb AAP83387.1	euFUL FRUITFULL-like MADS-box [P...	39	0.026
gi 32478011 gb AAP83367.1	FRUITFULL-like MADS-box [Clarkia...	39	0.030
gi 27372825 dbj BAC53738.1	PnSAH1 [Ipomoea nil]	39	0.031

## Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|18424410|ref|NP\_568929.1| MADS-box protein [Arabidopsis thaliana]  
gi|3912998|sp|Q38876|AGL8\_ARATH Agamous-like MADS box protein AGL8 (Floral homeot  
(Transcription factor FRUITFULL)  
gi|2129536|pir|S71208 MADS box protein AGL8 - Arabidopsis thaliana  
gi|1004365|gb|AAA97403.1| AGL8  
gi|10177314|dbj|BAB10640.1| floral homeotic protein AGL8 [Arabidopsis thaliana]  
gi|14423384|gb|AAK62374.1| floral homeotic protein AGL8 [Arabidopsis thaliana]  
gi|18377424|gb|AAL66878.1| floral homeotic protein AGL8 [Arabidopsis thaliana]  
Length = 242

Score = 68.9 bits (167), Expect = 2e-11

Identities = 34/34 (100%), Positives = 34/34 (100%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34

STDSCMERILERYDRYLYSDKQLVGRDVSQSENW

Sbjct: 58 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 91

☐ >gi|23304674|emb|CAD47850.1| MADS-box protein FUL-b [Brassica oleracea var. boti  
Length = 241

Score = 68.6 bits (166), Expect = 3e-11

Identities = 32/34 (94%), Positives = 34/34 (100%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34

STDSCMERILERYDRYLYSDKQLVGR++SQSENW

Sbjct: 58 STDSCMERILERYDRYLYSDKQLVGREISQSENW 91

☐ >gi|3913000|sp|Q41274|AGL8\_SINAL Agamous-like MADS box protein AGL8 homolog (MAI  
gi|1049024|gb|AAB41525.1| transcription factor SaMADS B  
Length = 241

Score = 67.8 bits (164), Expect = 5e-11  
Identities = 32/34 (94%), Positives = 34/34 (100%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
STDSCME+ILERYDRYLYSDKQLVGRD+SQSENW  
Sbjct: 58 STDSCMEKILERYDRYLYSDKQLVGRDISQSENW 91

☐ >gi|23304676|emb|CAD47851.1| MADS-box protein FUL-c [Brassica oleracea var. botrytis]  
Length = 243

Score = 65.5 bits (158), Expect = 3e-10  
Identities = 32/34 (94%), Positives = 33/34 (97%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
STDSCMERILERYDRYLYSDKQLVGRD+SQSENW  
Sbjct: 58 STDSSMERILERYDRYLYSDKQLVGRDISQSENW 91

☐ >gi|23304678|emb|CAD47852.1| MADS-box protein FUL-d [Brassica oleracea var. botrytis]  
Length = 242

Score = 65.5 bits (158), Expect = 3e-10  
Identities = 32/34 (94%), Positives = 33/34 (97%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
STDSCMERILERYDRYLYSDKQLVGRD+SQSENW  
Sbjct: 58 STDSSMERILERYDRYLYSDKQLVGRDISQSENW 91

☐ >gi|23304672|emb|CAD47849.1| MADS-box protein FUL-a [Brassica oleracea var. botrytis]  
Length = 239

Score = 65.1 bits (157), Expect = 3e-10  
Identities = 31/34 (91%), Positives = 32/34 (94%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
STDSCME ILERYDRYLYSDKQLVGRD+SQ ENW  
Sbjct: 56 STDSCMESILERYDRYLYSDKQLVGRDISQIENW 89

☐ >gi|1483232|emb|CAA67969.1| MADS5 protein [Betula pendula]  
Length = 244

Score = 50.4 bits (119), Expect = 8e-06  
Identities = 22/34 (64%), Positives = 29/34 (85%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
STDSCMERILERY+RY Y+D+QL+ D+ Q+ +W  
Sbjct: 58 STDSCMERILERYERYSYADRQLLANDLEQNGSW 91

☐ >gi|13446154|emb|CAC35027.1| MADS-box transcription factor [Pisum sativum]  
 gi|13661024|emb|CAC37031.1| MADS-box transcription factor [Pisum sativum]  
 gi|18252655|gb|AAL66379.1| MADS-box transcription factor MADS4 [Pisum sativum]  
 Length = 240

Score = 46.6 bits (109), Expect = 1e-04  
 Identities = 20/34 (58%), Positives = 26/34 (76%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
 +TDSCME+ILERY+RY Y+++QLV D NW  
 Sbjct: 58 ATDSCMEKILERYERYSYAERQLVANDSESQGNW 91

☐ >gi|32478063|gb|AAP83393.1| euFUL FRUITFULL-like MADS-box [Pisum sativum]  
 Length = 199

Score = 46.2 bits (108), Expect = 2e-04  
 Identities = 21/34 (61%), Positives = 27/34 (79%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
 S+D CMERILERY+RY Y+++Q V D Q+ENW  
 Sbjct: 23 SSDPCMERILERYERYSYAERQHVPNDQPQENW 56

☐ >gi|16162|emb|CAA78909.1| AP1 [Arabidopsis thaliana]  
 Length = 255

Score = 45.4 bits (106), Expect = 3e-04  
 Identities = 19/34 (55%), Positives = 27/34 (79%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
 STDSCME+ILERY+RY Y+++QL+ + + NW  
 Sbjct: 58 STDSCMEKILERYERYSYAERQLIAPESDVNTNW 91

☐ >gi|28381535|gb|AAF12699.2| PTM1 [Populus tremuloides]  
 Length = 248

Score = 45.4 bits (106), Expect = 3e-04  
 Identities = 19/34 (55%), Positives = 25/34 (73%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
 STD CME ILERY+RY Y+++QLV D+ +W  
 Sbjct: 58 STDDCMEEILERYERYSYAERQLVATDLDSQGDW 91

☐ >gi|14518447|gb|AAF22139.2| MADS box protein [Capsicum annuum]  
 Length = 247

Score = 45.4 bits (106), Expect = 3e-04  
 Identities = 21/34 (61%), Positives = 26/34 (76%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
 STDSCMERILERY+RY Y+++QL DV +W

Sbjct: 58 STDSCMERILERYERYSYAERQLNATDVETPGSW 91

☐ >gi|15222220|ref|NP\_177074.1| floral homeotic gene APETALA1 [Arabidopsis thaliana]  
 gi|21542380|sp|P35631|AP1\_ARATH Floral homeotic protein APETALA1 (Agamous-like MA  
 AGL7)  
 gi|478713|pir|S27109 MADS box protein AP1 - Arabidopsis thaliana  
 gi|6730649|gb|AAF27070.1| F4N2.9 [Arabidopsis thaliana]  
 gi|28393428|gb|AAO42136.1| putative floral homeotic protein APETALA1 [Arabidopsis  
 gi|28827280|gb|AAO50484.1| putative floral homeotic protein APETALA1 [Arabidopsis  
 gi|383297|prf|1902329A APETALA1 gene  
 Length = 256

Score = 45.1 bits (105), Expect = 3e-04  
 Identities = 19/34 (55%), Positives = 27/34 (79%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
 STDSCME+ILERY+RY Y+++QL+ + + NW  
 Sbjct: 58 STDSCMEKILERYERYSYAERQLIAPESDVNTNW 91

☐ >gi|20799348|gb|AAM28451.1| apetala 1 [Arabidopsis thaliana]  
 Length = 251

Score = 45.1 bits (105), Expect = 4e-04  
 Identities = 19/34 (55%), Positives = 27/34 (79%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
 STDSCME+ILERY+RY Y+++QL+ + + NW  
 Sbjct: 58 STDSCMEKILERYERYSYAERQLIAPESDVNTNW 91

☐ >gi|6634708|gb|AAF19721.1| MADS box transcription factor [Petunia x hybrida]  
 Length = 246

Score = 45.1 bits (105), Expect = 4e-04  
 Identities = 21/34 (61%), Positives = 27/34 (79%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
 +TDSCMERILERY+RY Y+++QLV D S +W  
 Sbjct: 58 ATDSCMERILERYERYSYAERQLVSTDHSSPGSW 91

☐ >gi|3646320|emb|CAA04321.1| MADS-box protein [Malus x domestica]  
 Length = 239

Score = 44.7 bits (104), Expect = 4e-04  
 Identities = 20/34 (58%), Positives = 26/34 (76%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
 +TDSCME+ILERY+RY Y+++QLV D NW  
 Sbjct: 58 ATDSCMEQILERYERYSYAERQLVEPDFESQGNW 91

☐ >gi|32478021|gb|AAP83372.1| euAP1 APETALA1-like MADS-box [Heuchera americana]  
Length = 236

Score = 44.7 bits (104), Expect = 4e-04  
Identities = 20/34 (58%), Positives = 26/34 (76%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
STDSCME+ILERY+RY Y++++LV ENW

Sbjct: 53 STDSCMEKILERYERYSYAERRLVATGSESQSENW 86

☐ >gi|20799358|gb|AAM28456.1| apetala 1 [Arabidopsis thaliana]  
Length = 251

Score = 44.7 bits (104), Expect = 4e-04  
Identities = 19/34 (55%), Positives = 27/34 (79%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
STDSCME+ILERY+RY Y+++QL+ + + NW

Sbjct: 58 STDSCMEKILERYERYSYAERQLIAPESDVNTNW 91

☐ >gi|20799344|gb|AAM28449.1| apetala 1 [Arabidopsis thaliana]  
Length = 251

Score = 44.7 bits (104), Expect = 4e-04  
Identities = 19/34 (55%), Positives = 27/34 (79%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
STDSCME+ILERY+RY Y+++QL+ + + NW

Sbjct: 58 STDSCMEKILERYERYSYAERQLIAPEDVNTNW 91

☐ >gi|20799346|gb|AAM28450.1| apetala 1 [Arabidopsis thaliana]  
Length = 251

Score = 44.7 bits (104), Expect = 5e-04  
Identities = 19/34 (55%), Positives = 27/34 (79%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
STDSCME+ILERY+RY Y+++QL+ + + NW

Sbjct: 58 STDSCMEKILERYERYSYAERQLIAPESDVNTNW 91

☐ >gi|20799340|gb|AAM28447.1| apetala 1 [Arabidopsis thaliana]  
gi|20799342|gb|AAM28448.1| apetala 1 [Arabidopsis thaliana]  
gi|20799350|gb|AAM28452.1| apetala 1 [Arabidopsis thaliana]  
gi|20799352|gb|AAM28453.1| apetala 1 [Arabidopsis thaliana]  
gi|20799354|gb|AAM28454.1| apetala 1 [Arabidopsis thaliana]  
gi|20799356|gb|AAM28455.1| apetala 1 [Arabidopsis thaliana]  
gi|20799360|gb|AAM28457.1| apetala 1 [Arabidopsis thaliana]  
gi|20799366|gb|AAM28460.1| apetala 1 [Arabidopsis thaliana]  
gi|20799368|gb|AAM28461.1| apetala 1 [Arabidopsis thaliana]  
Length = 251

Score = 44.7 bits (104), Expect = 5e-04  
Identities = 19/34 (55%), Positives = 27/34 (79%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
STDSCME+ILERY+RY Y+++QL+ + + NW  
Sbjct: 58 STDSCMEKILERYERYSYAERQLIAPESDVNTNW 91

☐ >gi|20799362|gb|AAM28458.1| apetala 1 [Arabidopsis thaliana]  
Length = 251

Score = 44.7 bits (104), Expect = 5e-04  
Identities = 19/34 (55%), Positives = 27/34 (79%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
STDSCME+ILERY+RY Y+++QL+ + + NW  
Sbjct: 58 STDSCMEKILERYERYSYAERQLIAPESDVNTNW 91

☐ >gi|20799364|gb|AAM28459.1| apetala 1 [Arabidopsis thaliana]  
Length = 251

Score = 44.7 bits (104), Expect = 5e-04  
Identities = 19/34 (55%), Positives = 27/34 (79%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
STDSCME+ILERY+RY Y+++QL+ + + NW  
Sbjct: 58 STDSCMEKILERYERYSYAERQLIAPESDVNTNW 91

☐ >gi|27657753|gb|AAO18232.1| MADS-box transcriptional factor HAM92 [Helianthus ar  
Length = 251

Score = 44.3 bits (103), Expect = 5e-04  
Identities = 20/29 (68%), Positives = 24/29 (82%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVS 29  
STDSCME ILERY+RY YS++QLV D +  
Sbjct: 58 STDSCMESILERYERYCYSERQLVATDAT 86

☐ >gi|21593537|gb|AAM65504.1| homeotic protein boilAP1, putative [Arabidopsis tha  
Length = 256

Score = 44.3 bits (103), Expect = 5e-04  
Identities = 19/34 (55%), Positives = 27/34 (79%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
STDSCME+ILERY+RY Y+++QL+ + + NW  
Sbjct: 58 STDSCMEKILERYERYSYAERQLIAPESDVNTNW 91

☐ >gi|32478037|gb|AAP83380.1| euFUL FRUITFULL-like MADS-box [*Lycopersicon esculent*]  
Length = 210

Score = 44.3 bits (103), Expect = 5e-04  
Identities = 20/34 (58%), Positives = 26/34 (76%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
STDSCMERILERY+RY Y+++QL D+ +W  
Sbjct: 25 STDSCMERILERYERYSYAERQLNATDIITPGSW 58

☐ >gi|602906|emb|CAA56658.1| SLM4 [*Silene latifolia*]  
Length = 246

Score = 44.3 bits (103), Expect = 5e-04  
Identities = 19/34 (55%), Positives = 25/34 (73%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
++DSCME+ILERY+RY Y++KQL D NW  
Sbjct: 58 ASDSCMEKILERYERYCYAEKQLASNDPDAQVNW 91

☐ >gi|32478017|gb|AAP83370.1| euAP1 APETALA1-like MADS-box [*Corylopsis sinensis*]  
Length = 218

Score = 44.3 bits (103), Expect = 6e-04  
Identities = 20/33 (60%), Positives = 26/33 (78%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSEN 33  
STDSCME+ILERY+RY Y+++QLV D + N  
Sbjct: 32 STDSCMEKILERYERYSYAERQLVATDPNSQGN 64

☐ >gi|4416347|gb|AAD20329.1| MADS C-2 protein; MADS-box protein [*Sinapis alba*]  
Length = 254

Score = 44.3 bits (103), Expect = 6e-04  
Identities = 19/34 (55%), Positives = 27/34 (79%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
STDSCME+ILERY+RY Y+++QL+ + + NW  
Sbjct: 58 STDSCMEKILERYERYSYAERQLIAPESDSNTNW 91

☐ >gi|82313|pir||S20886 MADS box protein squa - garden snapdragon  
gi|16052|emb|CAA45228.1| SQUA [*Antirrhinum majus*]  
Length = 248

Score = 43.9 bits (102), Expect = 7e-04  
Identities = 18/34 (52%), Positives = 26/34 (76%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
STDSCM+RILE+Y+RY ++++QLV + NW  
Sbjct: 58 STDSCMDRILEKYERYSFARQLVSNPQSPANW 91



☐ >gi|1561780|gb|AAB08876.1| homeotic protein boi2AP1 [Brassica oleracea]  
gi|23304680|emb|CAD47853.1| MADS-box protein AP1-a [Brassica oleracea var. botryt]  
Length = 256

Score = 43.9 bits (102), Expect = 7e-04  
Identities = 19/34 (55%), Positives = 27/34 (79%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
STDSCME+ILERY+RY Y+++QL+ + + NW  
Sbjct: 58 STDSCMEKILERYERYSYAERQLIAPESDSNTNW 91

☐ >gi|32478023|gb|AAP83373.1| FRUITFULL-like MADS-box [Heuchera americana]  
Length = 216

Score = 43.9 bits (102), Expect = 8e-04  
Identities = 19/34 (55%), Positives = 25/34 (73%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
STDS ME+ILERY+RY Y+++QL+ D NW  
Sbjct: 25 STDSSMEKILERYERYSYAERQLIATDSELQGNW 58

☐ >gi|1561778|gb|AAB08875.1| homeotic protein boilAP1 [Brassica oleracea]  
gi|23304682|emb|CAD47854.1| MADS-box protein AP1-c [Brassica oleracea var. botryt]  
Length = 256

Score = 43.9 bits (102), Expect = 8e-04  
Identities = 19/34 (55%), Positives = 27/34 (79%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
STDSCME+ILERY+RY Y+++QL+ + + NW  
Sbjct: 58 STDSCMEKILERYERYSYAERQLIAPESDVNTNW 91

☐ >gi|28381537|gb|AAF12700.2| PTM2 [Populus tremuloides]  
Length = 240

Score = 43.9 bits (102), Expect = 8e-04  
Identities = 18/34 (52%), Positives = 27/34 (79%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
ST++CME+ILER++RY Y+++QLV D+ NW  
Sbjct: 58 STNACMEKILERHERYSYAERQLVATDLDSQGNW 91

☐ >gi|4102111|gb|AAD01421.1| NAP1-1 [Nicotiana tabacum]  
Length = 245

Score = 43.5 bits (101), Expect = 9e-04  
Identities = 20/34 (58%), Positives = 25/34 (73%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
 STDSCMERILERY+RY Y+++QL D +W  
 Sbjct: 58 STDSCMERILERYERYSYAERQLTATDHETPGSW 91

☐ >gi|32478045|gb|AAP83384.1| euAP1 APETALA1-like MADS-box [Phytolacca americana]  
 Length = 239

Score = 43.5 bits (101), Expect = 9e-04  
 Identities = 19/34 (55%), Positives = 25/34 (73%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
 STDS ME+ILERY+RY Y+++QL D + NW  
 Sbjct: 53 STDSSMEKILERYERYFYAERQLASNDPNTENVN 86

☐ >gi|6707086|gb|AAF25589.1| apetalal [Arabidopsis lyrata]  
 gi|20799370|gb|AAM28462.1| apetala 1 [Arabidopsis lyrata]  
 Length = 251

Score = 43.5 bits (101), Expect = 0.001  
 Identities = 19/34 (55%), Positives = 27/34 (79%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
 STDSCME+ILERY+RY Y+++QL+ + + NW  
 Sbjct: 58 STDSCMEKILERYERYSYAERQLIAPESDVNTNW 91

☐ >gi|29372764|emb|CAD23417.1| m4 [Zea mays]  
 Length = 245

Score = 43.5 bits (101), Expect = 0.001  
 Identities = 18/34 (52%), Positives = 25/34 (73%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
 STDSCM++ILERY+RY Y++K L+ + NW  
 Sbjct: 58 STDSCMDKILERYERYSYAEKVLISAEYETQGNW 91

☐ >gi|3913047|sp|Q41276|AP1\_SINAL Floral homeotic protein APETALA1 (MADS C)  
 gi|1076477|pir||S52236 MADS box protein ap1 - white mustard  
 gi|609253|emb|CAA57233.1| Saap1 [Sinapis alba]  
 Length = 254

Score = 43.5 bits (101), Expect = 0.001  
 Identities = 19/34 (55%), Positives = 27/34 (79%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
 STDSCME+ILERY+RY Y+++QL+ + + NW  
 Sbjct: 58 STDSCMEKILERYERYSYAERQLIAPESDVNTNW 91

☐ >gi|3947985|gb|AAC83170.1| MADS-box protein 2 [Malus x domestica]  
Length = 255

Score = 43.5 bits (101), Expect = 0.001  
Identities = 19/34 (55%), Positives = 26/34 (76%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
S DSCMERILERY+RY Y+++QL+ D + +W  
Sbjct: 58 SNDSCMERILERYERYSYTERQLLANDNESTGSW 91

☐ >gi|32478095|gb|AAP83409.1| euAP1 APETALA1-like MADS-box [Syringa vulgaris]  
Length = 210

Score = 43.1 bits (100), Expect = 0.001  
Identities = 17/34 (50%), Positives = 26/34 (76%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
+TDSCM+RILE+Y+RY +++QLV + NW  
Sbjct: 23 ATDSCMDRILEKYERYSFARQLVTNEPQSPANW 56

☐ >gi|3912987|sp|O22328|AGL8\_SOLCO Agamous-like MADS box protein AGL8 homolog  
gi|7446507|pir|T07902 MADS box protein - Commerson's wild potato  
gi|2290778|gb|AAB65161.1| MADS box transcription factor [Solanum commersonii]  
Length = 250

Score = 43.1 bits (100), Expect = 0.001  
Identities = 19/34 (55%), Positives = 27/34 (79%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
+TDSCMER+LERY+RY +++KQLV D + +W  
Sbjct: 58 ATDSCMERLLERYERYSFARQLVPTDHTSPGSW 91

☐ >gi|602908|emb|CAA56659.1| SLM5 [Silene latifolia]  
Length = 257

Score = 43.1 bits (100), Expect = 0.001  
Identities = 18/34 (52%), Positives = 25/34 (73%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
+TDSCME+ILERY+RY Y+++QL D +W  
Sbjct: 58 ATDSCMEKILERYERYSYAERQLTAPDPDSHVSW 91

☐ >gi|5070142|gb|AAD39036.1| MADS-box protein MADS1 [Nicotiana sylvestris]  
Length = 245

Score = 43.1 bits (100), Expect = 0.001  
Identities = 20/34 (58%), Positives = 25/34 (73%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
STDSCMERILERY+RY Y+++QL D +W

Sbjct: 58 STDSCMERILERYERYSYAERQLTATDDETPGSW 91

☐ >gi|27804355|gb|AAO22979.1| MADS-box transcription factor CDM111 [Chrysanthemum]  
Length = 246

Score = 42.7 bits (99), Expect = 0.001  
Identities = 19/29 (65%), Positives = 24/29 (82%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVS 29  
STDSCME ILERY+RY Y+++QLV D +  
Sbjct: 58 STDSCMESILERYERYSYTERQLVATDAT 86

☐ >gi|27373049|gb|AAO12211.1| MADS11 [Nicotiana tabacum]  
Length = 245

Score = 42.7 bits (99), Expect = 0.002  
Identities = 20/34 (58%), Positives = 25/34 (73%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
STDSCMERILERY+RY Y+++QL D +W  
Sbjct: 58 STDSCMERILERYERYSYAERQLTATDHETPGSW 91

☐ >gi|30580167|sp|Q39081|CAL\_ARATH Transcription factor CAULIFLOWER (Agamous-like  
AGL10)  
Length = 253

Score = 42.4 bits (98), Expect = 0.002  
Identities = 17/34 (50%), Positives = 27/34 (79%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
S++SCME++LERY+RY Y+++QL+ D + NW  
Sbjct: 58 SSESCMEKVLERYERYSYAERQLIAPDSHVNTNW 91

☐ >gi|27542946|gb|AAO16552.1| apetala 1-like protein [Metrosideros excelsa]  
Length = 119

Score = 42.4 bits (98), Expect = 0.002  
Identities = 16/34 (47%), Positives = 27/34 (79%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
+TD+CME+ILERY+RY Y+++Q++ + + NW  
Sbjct: 46 ATDACMEKILERYERYSYAERQILTNNATNGNW 79

☐ >gi|11120557|gb|AAG30923.1| MADS box protein AP2L [Eucalyptus globulus]  
Length = 245

Score = 42.4 bits (98), Expect = 0.002  
Identities = 17/34 (50%), Positives = 25/34 (73%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
 +TD CMERILERY+RY Y++ Q++ + + NW  
 Sbjct: 58 ATDCCMERILERYERYSYAESQVLTTNAETNGNW 91

☐ >gi|22091473|emb|CAC81068.1| MADS box transcription factor [Daucus carota subsp.  
 Length = 242

Score = 42.4 bits (98), Expect = 0.002  
 Identities = 18/34 (52%), Positives = 25/34 (73%)

Query: 1 STDSCMERILERYDRYLYSDKQLVGRDVSQSENW 34  
 STDS ME ILERY+RY Y+++Q++ D + NW  
 Sbjct: 58 STDSSMEEILERYERYSYAERQVIANDPESTGNW 91

Get selected sequences

Select all

Deselect all

Database: All non-redundant GenBank CDS  
 translations+PDB+SwissProt+PIR+PRF  
 Posted date: Dec 18, 2003 12:38 AM  
 Number of letters in database: 517,909,209  
 Number of sequences in database: 1,580,593

Lambda	K	H
0.315	0.131	0.390

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 7,984,363

Number of Sequences: 1580593

Number of extensions: 164489

Number of successful extensions: 377

Number of sequences better than 10.0: 32

Number of HSP's better than 10.0 without gapping: 32

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 345

Number of HSP's gapped (non-prelim): 32

length of query: 34

length of database: 517,909,209

effective HSP length: 10

effective length of query: 24

effective length of database: 502,103,279

effective search space: 12050478696

effective search space used: 12050478696

T: 11

A: 40

X1: 16 ( 7.3 bits)

X2: 38 (14.6 bits)

•  
X3: 64 (24.7 bits)  
S1: 41 (21.6 bits)  
S2: 67 (30.4 bits)